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OM protein - protein search, using sw model

Run on: September 10, 2003, 09:26:53 ; Search time 47 Seconds
(without alignments)
3934.393 Million cell updates/sec

Title: US-09-834-792C-4

Perfect score: 6091
Sequence: 1 MOVQGRPGSPGDAEDRRE.....HRGIDGQPGAGQPPSDT 1165

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1980.DAT.*
2: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1991.DAT.*
3: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1992.DAT.*
4: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA1993.DAT.*
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21: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneeq/geneeq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6073	99.7	1165	22	Human MTR1 protein
2	6073	99.7	1165	23	Human TRP8
3	6073	99.7	1165	23	Human TRP8
4	6014	98.7	1179	22	Human MTR1 protein
5	5068.5	83.2	1158	22	Mouse MTR1 protein
6	5068.5	83.2	1158	22	Mouse TRP8
7	5068.5	83.2	1158	22	Mouse MTR1 protein
8	5053	83.0	1157	23	Mouse TRP8
9	4988.5	81.9	1164	23	Rat L-TRP SEQ ID N

10	4523	74.3	872	22	Human MTR1 protein
11	2430.5	39.9	1166	23	Prostate cancer-as
12	2430.5	39.9	1214	23	Human calcium chan
13	2426.5	39.8	1214	23	Human TRP9 protein
14	2394.5	39.3	1129	22	Human TRP8
15	2335	38.3	1083	24	Human TRP8
16	2166.5	35.6	1040	23	Human secreted pro
17	2146	35.2	1016	23	Human secreted pro
18	2041	33.5	1503	21	Human putative Ca2
19	2041	33.5	1503	21	Human TRP8
20	2041	33.5	1503	21	Human TRP8
21	2041	33.5	1503	23	Human TRP8
22	2041	33.5	1503	23	Human TRP8
23	1601	26.3	725	21	Human TRP8
24	1587.5	26.1	725	21	Human TRP8
25	1570.5	25.8	1104	21	Human TRP8
26	1562.5	25.7	1095	20	Human TRP8
27	1562.5	25.7	1095	22	Human TRP8
28	1562.5	25.7	1095	22	Human TRP8
29	1562.5	25.7	1095	22	Human TRP8
30	1562.5	25.7	1095	24	Human TRP8
31	1559.5	25.6	1104	23	Human TRP8
32	1554.5	25.5	1095	22	Human TRP8
33	1554.5	25.5	1095	22	Human TRP8
34	1554.5	25.5	1095	22	Human TRP8
35	1554.5	25.5	1095	22	Human TRP8
36	1481	24.3	665	19	Human TRP8
37	1481	24.3	665	21	Human TRP8
38	1316.5	21.6	1707	24	Human TRP8
39	1305.5	21.4	1172	23	Human TRP8
40	1300.5	21.4	1162	22	Human TRP8
41	1300.5	21.4	1172	22	Human TRP8
42	1300.5	21.4	1544	22	Human TRP8
43	1300.5	21.4	1554	22	Human TRP8
44	1293	21.2	1187	22	Human TRP8
45	1293	21.2	1197	22	Human TRP8

ALIGNMENTS

RESULT 1	AA86162	standard; Protein: 1165 AA.
XX	AA86162;	
AC	09-AUG-2001	(first entry)
XX		
DT		
XX		
DE		
XX		
KM	Human MTR1 protein containing exon 18 fragment.	
KM	MTR1, TRP-related protein; Ca2+ regulation; calcium regulation; tumor;	
KM	transient receptor potential family; BWS; Beckwith-Wiedemann syndrome;	
KM	11p15.5 abnormality; chromosome 11; anticancer; developmental activity;	
KM	intracellular calcium ion regulation; hormone; growth factor; apoptosis;	
KM	cell growth; cell death; cell differentiation; urogenital disease;	
KM	polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;	
KM	rhabdomyosarcoma.	
OS	Homo sapiens.	
XX		
PN	WO200132693-A2.	
XX		
PD	10-MAY-2001.	
XX		
PF	06-NOV-2000; 2000MO-DE03876.	
XX		
PR	04-NOV-1999; 99DE-1053167.	
XX		
PA	(UTG-) UNIV GUTENBERG JOHANNES.	
XX		
PI	Prawitt D, Pelletier J, Zabel B;	
XX		

Antennaria
Protein

DR WPI: 2001-316417/33.
 DR N-PSDB: AAH20574.
 XX
 PT DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
 PT syndrome and tumors, also related proteins and antibodies -
 XX
 PS
 XX
 Claim 10; Fig 4; 46pp; German.

This invention describes a novel DNA sequence (I) encoding the MTR1 protein that: (i) has at least one biological activity of a TRP (transient receptor potential) family protein; (ii) is connected with etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected with tumors involving 11p15.5 abnormalities. The products of the invention have anticancer and developmental activity. MTR1 is involved in regulation of intracellular calcium ion levels, which are essential for cellular responses to hormones and/or growth factors; also in apoptosis and cell growth, death and differentiation, and in uterine diseases, including polycystic kidney disease. (I) and related ribozymes, antisense RNA, proteins and antibodies (Ab) are used to treat or prevent diseases associated with altered expression of the MTR1 gene or activity of its protein, or with calcium influx into cells, e.g. BWS, Wilms tumor, thaboid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also used for diagnosis of such diseases. (I) can also be used for recombinant production of MTR1 proteins (II) (used for analysis, characterization and therapy), as tissue or chromosomal markers, for identifying genetic diseases and related sequences, as primers for genetic fingerprinting, as source of oligonucleotides for biochips, and to raise anti-protein or anti-DNA antibodies. (II) are used to raise Ab, as reagents in competitive assays for (II), as tissue markers, for identifying interacting proteins and in screening for (anti)agonists. This sequence represents a human MTR1 protein described in the method of the invention.

Sequence 1165 AA;

Query Match 99.7%; Score 6073; DB 22; Length 1165;

Best Local Similarity 99.7%; Pred. No. 0;

Matches 1162; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MODVGGPRGPGDADREELGHRGEVAFGGSGKKRKFVRVPSGAVSFYFDLLAAW 60
 DB 1 MODVGGPRGPGDADREELGHRGEVAFGGSGKKRKFVRVPSGAVSFYFDLLAAW 60
 QY 61 HLPAPLVVSLVGEQGFAMKSLMDLVLRKGLVKAOSTGAMILTSALRGLARHVQAV 120
 DB 61 HLPAPLVVSLVGEQGFAMKSLMDLVLRKGLVKAOSTGAMILTSALRGLARHVQAV 120
 QY 121 RHSLASTSTKRVAVAGASLGRVLRHRIEBAQDFPVHYPEDDGSQGPLCSLDSNL 180
 DB 121 RHSLASTSTKRVAVAGASLGRVLRHRIEBAQDFPVHYPEDDGSQGPLCSLDSNL 180
 QY 181 SHPILVEPPPGKDGTLRLRLKGISEORAGVGSTSIETPVLCILVNDPNTLERI 240
 DB 181 SHPILVEPPPGKDGTLRLRLKGISEORAGVGSTSIETPVLCILVNDPNTLERI 240
 QY 241 SRAVEQAAMWLIVSGSGIADVLALVNPVPHLVPAEKOFEKEPSPKGFMSMEDIVMT 300
 DB 241 SRAVEQAAMWLIVSGSGIADVLALVNPVPHLVPAEKOFEKEPSPKGFMSMEDIVMT 300
 QY 301 KLLQNTSHOHLITVDFEQQSGSELDVYLKALVACSHSQSEPDYIDELKLAAMDR 360
 DB 301 KLLQNTSHOHLITVDFEQQSGSELDVYLKALVACSHSQSEPDYIDELKLAAMDR 360
 QY 361 VDIASEINFGDVEWMSCDLEVMVDALVSNKEPFRLLPVNDGADVADFLTGRLOELR 420
 DB 361 VDIASEINFGDVEWMSCDLEVMVDALVSNKEPFRLLPVNDGADVADFLTGRLOELR 420
 QY 421 SVSRKSLFDLLORKOEBARLTLAGLGTQOARPPAPPAFLSHESRYLKDPLQDACRG 480
 DB 421 SVSRKSLFDLLORKOEBARLTLAGLGTQOARPPAPPAFLSHESRYLKDPLQDACRG 480
 QY 481 FYQDGGPGRRRRAEKGPAPKPTGQKWLIDLINQSENPMWDLFLMAVLQNRHEMATYFWAM 540
 DB 481 FYQDGGPGRRRRAEKGPAPKPTGQKWLIDLINQSENPMWDLFLMAVLQNRHEMATYFWAM 540

QY 541 GQGVAAALAAACKILKEMSHLETEAARATREAKRYERLADLFSECSYSEARAFALLV 600
 DB 541 GQGVAAALAAACKILKEMSHLETEAARATREAKRYERLADLFSECSYSEARAFALLV 600
 QY 601 RNRKCSKTTGLHATEADAKAPFAHGVQVAFTRIRWGMMACTPIRLIGALFCPALV 660
 DB 601 RNRKCSKTTGLHATEADAKAPFAHGVQVAFTRIRWGMMACTPIRLIGALFCPALV 660
 QY 661 YTNLITSEEPALRTGLEDLODLSLDEKSPVGLGSRVSELYEAPRAGDRGRAVFL 720
 DB 661 YTNLITSEEPALRTGLEDLODLSLDEKSPVGLGSRVSELYEAPRAGDRGRAVFL 720
 QY 721 LTRNRKFGAVTVFLGVVWYFAFLFTYVLLVDFEPPPGSGSEPTLYFWFTLV 780
 DB 721 LTRNRKFGAVTVFLGVVWYFAFLFTYVLLVDFEPPPGSGSEPTLYFWFTLV 780
 QY 781 EIRQGFETDDETHLVKKFTLYVGDNNKCDMAIFLIVGTCRMLPSAFAGRTVLAM 840
 DB 781 EIRQGFETDDETHLVKKFTLYVGDNNKCDMAIFLIVGTCRMLPSAFAGRTVLAM 840
 QY 841 DEWFTTLHLIHLHQLGPKITVBERMKDVEPFLFSLVWLVAVGTTQALLPHPDG 900
 DB 841 DEWFTTLHLIHLHQLGPKITVBERMKDVEPFLFSLVWLVAVGTTQALLPHPDG 900
 QY 901 RLEWIFRVLRYRPIQLFGQIPLDEIDARVNCSTHPLLEDSPCSPSLYANMLVILLY 960
 DB 901 RLEWIFRVLRYRPIQLFGQIPLDEIDARVNCSTHPLLEDSPCSPSLYANMLVILLY 960
 QY 961 TFLVTVNLVNLMLIAMSYFQVQGNATYFMKFORYNLIVEYHERPALAPPTLLSHL 1020
 DB 961 TFLVTVNLVNLMLIAMSYFQVQGNATYFMKFORYNLIVEYHERPALAPPTLLSHL 1020
 QY 1021 SLTLARVKEAHEKREHLERDLPDLOKXVYMETVCKENFLSMKERRRDSGEVLRX 1080
 DB 1021 SLTLARVKEAHEKREHLERDLPDLOKXVYMETVCKENFLSMKERRRDSGEVLRX 1080
 QY 1081 TAHRYDFIAKYLGLREDEKRIKCLSQINYSVLSVADVLAQGGPRSSOHGEGSQ 1140
 DB 1081 TAHRYDFIAKYLGLREDEKRIKCLSQINYSVLSVADVLAQGGPRSSOHGEGSQ 1140
 QY 1141 LVAADHRRGIDGWEQPGAGOPPSPDT 1165
 DB 1141 LVAADHRRGIDGWEQPGAGOPPSPDT 1165

RESULT 2
 ABB83855
 ID ABB83855 standard; Protein; 1165 AA.
 AC ABB83855;
 XX
 DT 30-SEP-2002 (first entry)
 XX
 DE Human ltrpc6 SEQ ID NO 8.
 XX
 KW Human; ltrpc6; taste; cell signalling; TC-1CS; food; pharmaceutical;
 XX taste cell-specific ion channel subunit.
 OS Homo sapiens.
 XX
 PN WO200254069-A1.
 XX
 PD 11-JUL-2002.
 XX
 PF 26-DEC-2001; 2001WO-US49808.
 XX
 PR 29-DEC-2000; 2000US-259379P.
 XX
 PR 21-DEC-2001; 2001US-0026188.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Zuker CS, Zhang Y;

Not available?

Shen

XX WPI: 2002-583632/62.
DR N-PSDB: ABRN85736.
PT Identifying modulators of taste signaling in taste cells for use in
PT food and pharmaceutical industries to customize and regulate taste, by
PT determining effect of the compound on a taste cell-specific ion channel
PT subunit
XX
PS Claim 1; Page 305; 306pp; English.
XX
CC The invention relates to identifying (M1) a compound that modulates taste
CC signaling in taste cells, by contacting the compound with a eukaryotic
CC host cell or cell membrane which expresses a taste cell-specific ion
CC channel subunit (TC-ICS), and determining a functional effect of the
CC compound upon a transmembrane ion flux of a predetermined ion.
CC Identifying a compound that modulates taste signaling in taste cells.
CC (M1) is useful for identifying a compound that binds to a taste cell
CC in taste cells, for identifying a compound that binds to a taste cell
CC specific ion channel subunit and for modulating taste signaling in taste
CC cells of a mammal, in particular a human. Modulators identified by (M1)
CC are used by the food and pharmaceutical industries to customize taste.
CC e.g. as additives to food or medicine so that the food or medicine tastes
CC different to the subject who ingests it. Bitter medicines can be made to
CC taste less bitter and sweet substance can be enhanced. The modulators are
CC useful for pharmacological and genetic modulation of taste signaling
CC pathways. The taste modulators can be directly administered to mammalian
CC subjects for modulation of taste in vivo. The present sequence is that of
CC the predicted human ttrpc6 protein of the invention.
XX
SQ Sequence 1165 AA;
Query Match 99.7%; Score 6073; DB 23; Length 1165;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1162; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MODVCGPPSPGDAEDREELGLHGEVNFSGSGKRGKRVVPSGVAHSVLFDDLLEW 60
DB 1 MODVCGPPSPGDAEDREELGLHGEVNFSGSGKRGKRVVPSGVAHSVLFDDLLEW 60
QY 61 HLPAPNLVSVLVGEEQPPAMKSWLMDVLRKGLVKAAGSTGAMLTSAARVGLARVGVANV 120
DB 61 HLPAPNLVSVLVGEEQPPAMKSWLMDVLRKGLVKAAGSTGAMLTSAARVGLARVGVANV 120
QY 121 RDHSLASTSTKRVVAVAGMASIGRVLRHRIIEBAEDFPVHYPPEDDGSOGPLGSDSNL 180
DB 121 RDHSLASTSTKRVVAVAGMASIGRVLRHRIIEBAEDFPVHYPPEDDGSOGPLGSDSNL 180
QY 181 SHFLIVEBPGPKGDLTELRLRLKHSIQRAGYGTGSIIEPVLCLLVNGDPPTLERI 240
DB 181 SHFLIVEBPGPKGDLTELRLRLKHSIQRAGYGTGSIIEPVLCLLVNGDPPTLERI 240
QY 241 SRAVEQAAPWILVSSGGIADVLALVNQPHILVVKVAEKQKFPSPKHSFMSDIIVMT 300
DB 241 SRAVEQAAPWILVSSGGIADVLALVNQPHILVVKVAEKQKFPSPKHSFMSDIIVMT 300
QY 301 KLLONITSHOHLITVYDFEAGESEELDTVILKALVKAKCKSHQSEODLDELKLAVAMDR 360
DB 301 KLLONITSHOHLITVYDFEAGESEELDTVILKALVKAKCKSHQSEODLDELKLAVAMDR 360
QY 361 VDIKSEIFNGDVEWKSCDLEEVVVDALVSNKPEFVRLFVNDGADVADFLTYGRLOELYR 420
DB 361 VDIKSEIFNGDVEWKSCDLEEVVVDALVSNKPEFVRLFVNDGADVADFLTYGRLOELYR 420
QY 421 SVSRKSLFLDLORQOEARLTLAGLGTQARREPPAGPAPASLHVSRYLKDPLDADRG 480
DB 421 SVSRKSLFLDLORQOEARLTLAGLGTQARREPPAGPAPASLHVSRYLKDPLDADRG 480
QY 481 FYQDGRPGDRRAEKGPAKPTGQKMLDLNOKSNPMRDPLFMAVVLNBRHEMATYFAM 540
DB 481 FYQDGRPGDRRAEKGPAKPTGQKMLDLNOKSNPMRDPLFMAVVLNBRHEMATYFAM 540
QY 541 GQGVAAALAAACKILKEMSHLETEAARATREAKYERLADLTFSECYNSSEARAFALLV 600

DB 541 GQGVAAALAAACKILKEMSHLETEAARATREAKYERLADLTFSECYNSSEARAFALLV 600
QY 601 RNRNCKSTTCLHATEADAKAPFAHDVQVFLRIRIMGDMAGPTILRLGAFICFALV 660
DB 601 RNRNCKSTTCLHATEADAKAPFAHDVQVFLRIRIMGDMAGPTILRLGAFICFALV 660
QY 661 YTNLITFSEEARLRTGLEDLDDLSLDTESKPSLYGLOSREVELYAPPAQDGRPAVFL 720
DB 661 YTNLITFSEEARLRTGLEDLDDLSLDTESKPSLYGLOSREVELYAPPAQDGRPAVFL 720
QY 721 LTRNRKFGAATVYPLGVNVMYFAFLFTYVLLVDFRPPQSGSGSEPTVLYFWFTVLV 780
DB 721 LTRNRKFGAATVYPLGVNVMYFAFLFTYVLLVDFRPPQSGSGSEPTVLYFWFTVLV 780
QY 781 EIRIOGPTDDBTLVKKFTLYVGDNNMKCMVAIFLIVGTORMLPSAREAGRTVLA 840
DB 781 EIRIOGPTDDBTLVKKFTLYVGDNNMKCMVAIFLIVGTORMLPSAREAGRTVLA 840
QY 841 DFMVFTLRLIIPAIHKGAPKIIIVERMKDVEFFLFSLVWLVAVGTTOALLHPHDG 900
DB 841 DFMVFTLRLIIPAIHKGAPKIIIVERMKDVEFFLFSLVWLVAVGTTOALLHPHDG 900
QY 901 RLEWIFRRVLYRPLYQIFGQIPLDEIDBARVNCSTHPLLEDSPSCPSLYANWLVILLV 960
DB 901 RLEWIFRRVLYRPLYQIFGQIPLDEIDBARVNCSTHPLLEDSPSCPSLYANWLVILLV 960
QY 961 TELLVNTVNLNMLIAMSSTFOVQVGNATMFMKFORNLIVYHERPALAPPTLLSHL 1020
DB 961 TELLVNTVNLNMLIAMSSTFOVQVGNATMFMKFORNLIVYHERPALAPPTLLSHL 1020
QY 1021 SLTLRVEKAEHREHLEBDLPPLDQKVYVETVQENFLSKMERGRDSEGEVLRK 1080
DB 1021 SLTLRVEKAEHREHLEBDLPPLDQKVYVETVQENFLSKMERGRDSEGEVLRK 1080
QY 1081 TAHAVDTIAKYLGLREGEKRIKCLSEQINYSVAVADVLAKGGPRSSQHGEGSQ 1140
DB 1081 TAHAVDTIAKYLGLREGEKRIKCLSEQINYSVAVADVLAKGGPRSSQHGEGSQ 1140
QY 1141 LVAADHRCIDGWEOPGAGPPSDT 1165
DB 1141 LVAADHRCIDGWEOPGAGPPSDT 1165
RESULT 3
ID AAM51708 standard; Protein, 1165 AA.
XX AAM51708;
XX 16-JAN-2002 (first entry)
XX Human TRP8.
XX Mouse; human; TRP8; transient receptor potential channel;
XX taste receptor cell; bitter; sweet; flavour enhancer; food; beverage;
XX pharmaceutical.
XX Homo sapiens.
XX WQ200179448-A2.
XX 25-OCT-2001.
XX 17-APR-2001; 2001WO-US12608.
XX 17-APR-2000; 2000US-197491P.
XX 13-APR-2001; 2001US-0834792.
XX (MOUN) MOUNT SINAI SCHOOL MEDICINE.
XX Margolskee RF, Huang L, Rong M, Max M, Perez CA;
XX

John's from 2/25

DR WPI: 2002-017608/02.
DR N-PSDB: AA199708.

A new transient receptor potential channel, designated TRP8, is expressed in taste receptor cells and associated with perception of bitter and sweet taste, and is useful to find new flavour enhancers.

Claim 9; Fig 4; 55pp; English.

The invention relates to a mouse and human transient receptor potential channel, TRP8, expressed in taste receptor cells and associated with the perception of bitter and sweet taste. Modulators of TRP8 are useful as flavour enhancers in foods, beverages and pharmaceuticals.

Sequence 1165 AA

Query Match 99.7%; Score 6073; DB 23; Length 1165;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1162; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 MODVGGPRGSGDADREELGLHGEVNFSGSGKKRGKRVPSGVAPVFDLLAEW 60
1 MODVGGPRGSGDADREELGLHGEVNFSGSGKKRGKRVPSGVAPVFDLLAEW 60
61 HLPAPNLVSLVGEOPFAMKSMRLDVLKGLVKAQSTGAWILTSALRVGLARHYGQAV 120
61 HLPAPNLVSLVGEOPFAMKSMRLDVLKGLVKAQSTGAWILTSALRVGLARHYGQAV 120
61 HLPAPNLVSLVGEOPFAMKSMRLDVLKGLVKAQSTGAWILTSALRVGLARHYGQAV 120
121 RDHSLASTSTKRVVAVAGNASLGRVLRHRIIEBAQDFPVHYPEDDGSQGPLCSLDSNL 180
121 RDHSLASTSTKRVVAVAGNASLGRVLRHRIIEBAQDFPVHYPEDDGSQGPLCSLDSNL 180
121 RDHSLASTSTKRVVAVAGNASLGRVLRHRIIEBAQDFPVHYPEDDGSQGPLCSLDSNL 180
181 SHFIIIVEPPPKGSGITELRLERKHISEORAGCGTSTIPVLCILVNGDPTLERTI 240
181 SHFIIIVEPPPKGSGITELRLERKHISEORAGCGTSTIPVLCILVNGDPTLERTI 240
181 SHFIIIVEPPPKGSGITELRLERKHISEORAGCGTSTIPVLCILVNGDPTLERTI 240
241 SRAVEQAAPWMLILVSGGIADVLALVNOPLVLPVAKOKEPKPKHFMEDIVMT 300
241 SRAVEQAAPWMLILVSGGIADVLALVNOPLVLPVAKOKEPKPKHFMEDIVMT 300
241 SRAVEQAAPWMLILVSGGIADVLALVNOPLVLPVAKOKEPKPKHFMEDIVMT 300
301 KLLQNTSHQHLITVYDFEQSSEELDTVILKALVACKSHSQEPDVIDELKLAVAMDR 360
301 KLLQNTSHQHLITVYDFEQSSEELDTVILKALVACKSHSQEPDVIDELKLAVAMDR 360
301 KLLQNTSHQHLITVYDFEQSSEELDTVILKALVACKSHSQEPDVIDELKLAVAMDR 360
361 VLIASEIENGVEWMSCDLEEMVDALVSNKPEFRLVNDGADVADLTITGRLOELVR 420
361 VLIASEIENGVEWMSCDLEEMVDALVSNKPEFRLVNDGADVADLTITGRLOELVR 420
361 VLIASEIENGVEWMSCDLEEMVDALVSNKPEFRLVNDGADVADLTITGRLOELVR 420
421 SVSRKSLFDLLQKOEERLTLAGLGTQOAREPPAPAFSLHEVSRYLKDPLDACRG 480
421 SVSRKSLFDLLQKOEERLTLAGLGTQOAREPPAPAFSLHEVSRYLKDPLDACRG 480
421 SVSRKSLFDLLQKOEERLTLAGLGTQOAREPPAPAFSLHEVSRYLKDPLDACRG 480
481 FYODGPGRRRAEKGPAPKPTGQKWLIDLNKSENPMWDLFLMAVLQNRHEMATYFWAM 540
481 FYODGPGRRRAEKGPAPKPTGQKWLIDLNKSENPMWDLFLMAVLQNRHEMATYFWAM 540
481 FYODGPGRRRAEKGPAPKPTGQKWLIDLNKSENPMWDLFLMAVLQNRHEMATYFWAM 540
541 GOGGVAALAAACKILKEMSHLETEAARATRAKTERIALDLFSSCYNSSEARAFALV 600
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541 GOGGVAALAAACKILKEMSHLETEAARATRAKTERIALDLFSSCYNSSEARAFALV 600
601 RNRNCSKTTCLHATEADAKAFPAHDGVOAFLTRIMGDMAAGTITLLGALFFAV 660
601 RNRNCSKTTCLHATEADAKAFPAHDGVOAFLTRIMGDMAAGTITLLGALFFAV 660
601 RNRNCSKTTCLHATEADAKAFPAHDGVOAFLTRIMGDMAAGTITLLGALFFAV 660
661 YTNLITFSEAPLRTGLDLDLSTESPLVGLQSRVEELVEAPRAQDGRPAVFL 720
661 YTNLITFSEAPLRTGLDLDLSTESPLVGLQSRVEELVEAPRAQDGRPAVFL 720
661 YTNLITFSEAPLRTGLDLDLSTESPLVGLQSRVEELVEAPRAQDGRPAVFL 720
721 LTRMRKFNAPVTVFLGNVVMYAFRLFITYVLVDFRPPQSPSEVTLFWVFTLV 780
721 LTRMRKFNAPVTVFLGNVVMYAFRLFITYVLVDFRPPQSPSEVTLFWVFTLV 780
721 LTRMRKFNAPVTVFLGNVVMYAFRLFITYVLVDFRPPQSPSEVTLFWVFTLV 780
781 BEIRQGFDEDETHLVKFFTLVGDNMNKCDAVAIFLFTVGTCTMLPSAFEAGRTVLAM 840

DB 781 BEIRQGFDEDETHLVKFFTLVGDNMNKCDAVAIFLFTVGTCTMLPSAFEAGRTVLAM 840
QY DEMFTLRLHIFAIHKOGLSKITVBERMMDVFPFLFELSVMLVAVGVTTQALLHPDG 900
DB DEMFTLRLHIFAIHKOGLSKITVBERMMDVFPFLFELSVMLVAVGVTTQALLHPDG 900
QY RLEWIFRRVLYRPLYQIPLDEIDARVNCSTHPLLEDSPSCPSLYANMLVILLV 960
DB RLEWIFRRVLYRPLYQIPLDEIDARVNCSTHPLLEDSPSCPSLYANMLVILLV 960
QY TFLVLTNVLNMLNLIAMSSTFYOVQGNFPMKFORNLVVEHERPALAPFLLSHL 1020
DB TFLVLTNVLNMLNLIAMSSTFYOVQGNFPMKFORNLVVEHERPALAPFLLSHL 1020
QY SUTLRVRVKEAEHREHLERDLPPLDQKVYVMTVOKENFLSMERRRDSEGEVLK 1080
DB SUTLRVRVKEAEHREHLERDLPPLDQKVYVMTVOKENFLSMERRRDSEGEVLK 1080
QY TAHRVDIAKYLGLREOEKIKLESQINYSVLVSVADVLAAQGGPRSSQHCESQ 1140
DB TAHRVDIAKYLGLREOEKIKLESQINYSVLVSVADVLAAQGGPRSSQHCESQ 1140
QY LVADHRCSTFGWBOPGAQPPSDT 1165
DB LVADHRCSTFGWBOPGAQPPSDT 1165
QY LVADHRCSTFGWBOPGAQPPSDT 1165
DB LVADHRCSTFGWBOPGAQPPSDT 1165

RESULT 4
AAB86165
ID AAB86165 standard; Protein; 1179 AA.
XX
AC AAB86165;
XX
DT 09-AUG-2001 (first entry)
XX
DE Human MTR1 protein.
XX
XX MTR1: TRP-related protein; Ca2+ regulation; calcium regulation; tumor;
XX transient receptor potential family; BMS; Beckwith-Wiedemann syndrome;
XX 11p15.5 abnormality; chromosome 11; anticancer; developmental activity;
XX intracellular calcium ion regulation; hormone; growth factor; apoptosis;
XX cell growth; cell death; cell differentiation; urogenital disease;
XX polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
XX rhabdomyosarcoma.
XX
OS Homo sapiens.
XX
PN WO200132693-A2.
XX
PD 10-MAY-2001.
XX
PF 06-NOV-2000; 2000MO-DE03876.
XX
PR 04-NOV-1999; 99DE-1053167.
XX
PA (UYGV-) UNIV GUTENBERG JOHANNES.
XX
PI Prawitt D, Pelletier J, Zabel B;
XX
DR WPI: 2001-316417/33.
XX
PT DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
XX syndrome and tumors, also related proteins and antibodies -
XX
PS Disclosure; Fig 12; 46pp; German.
XX
CC This invention describes a novel DNA sequence (I) encoding the MTR1
CC protein that: (i) has at least one biological activity of a TRP
CC (transient receptor potential) family protein; (ii) is connected with
CC etiology of BMS (Beckwith-Wiedemann syndrome) and/or (iii) is connected
CC with tumors involving 11p15.5 abnormalities. The products of the
CC invention have anticancer and developmental activity. MTR1 is involved in

regulation of intracellular calcium ion levels, which are essential for cellular responses to hormones and/or growth factors; also in apoptosis and cell growth, death and differentiation, and in urogenital diseases, including polycystic kidney disease. (i) and related ribozymes, antisense RNA, proteins and antibodies (Ab) are used to treat or prevent diseases associated with altered expression of the MTR1 gene or activity of its protein, or with calcium influx into cells, e.g. BMS, Wilms tumor, rhabdoid tumors and rhabdomyosarcoma. Probes from (i), or Ab, are also used for diagnosis of such diseases. (ii) can also be used for recombinant production of MTR1 proteins (ii) (used for analysis, characterization and therapy), as tissue or chromosomal markers, for identifying genetic diseases and related sequences, as primers for genetic fingerprinting, as source of oligonucleotides for biochips, and to raise anti-protein or anti-DNA antibodies. (ii) are used to raise Ab, as reagents in competitive assays for (ii), as tissue markers, for identifying interacting proteins and in screening for (ant)agonists. This sequence represents a human MTR1 protein described in the method of the invention.

Sequence 1179 AA;

Query Match 98.7%; Score 6014; DB 22; Length 1179;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1159; Conservative 1; Mismatches 4; Indels 16; Gaps 3;

QY 1 MODVQPPSPGDAEDRRELGLHGEVNFSGSGKRGKRYRVPDGVAPSVLPDLLAEW 60
DB 1 MODVQPPSPGDAEDRRELGLHGEVNFSGSGKRGKRYRVPDGVAPSVLPDLLAEW 60
QY 61 HLPAPNLVSLVGEBOPPAMKSWLRDYLKGLVKAOSTGAMILTSALRVLAAHVQAV 120
DB 61 HLPAPNLVSLVGEBOPPAMKSWLRDYLKGLVKAOSTGAMILTSALRVLAAHVQAV 120
QY 121 RDHSLASTSTYRVAVAGMAGSLGRVLRHRIIEAEOEDPPVYPEDDGGSGPLCSLSDNL 180
DB 121 RDHSLASTSTYRVAVAGMAGSLGRVLRHRIIEAEOEDPPVYPEDDGGSGPLCSLSDNL 180
QY 181 SHFLIVEBPFGPKDGLTELRLERKHISEQAGYGTGSIPIVLCILVNGDPTLERI 240
DB 181 SHFLIVEBPFGPKDGLTELRLERKHISEQAGYGTGSIPIVLCILVNGDPTLERI 240
QY 241 SRAVEOAPMILIVGSGGIAVLAALVNQPHLLVPKVAEKPFKEKPSKESMEDYRWT 300
DB 241 SRAVEOAPMILIVGSGGIAVLAALVNQPHLLVPKVAEKPFKEKPSKESMEDYRWT 300
QY 301 KLLONITSHOHLTYVDEPGSEELPTVILKALVKACKSHSOPDYLDELKLAVAMDR 360
DB 301 KLLONITSHOHLTYVDEPGSEELPTVILKALVKACKSHSOPDYLDELKLAVAMDR 360
QY 361 VDIKSEIFNGDVEMKSCDLEEVNDALVSNKPEFVRLFVNDGADVADFLTYGRLQELYR 420
DB 361 VDIKSEIFNGDVEMKSCDLEEVNDALVSNKPEFVRLFVNDGADVADFLTYGRLQELYR 420
QY 421 SVSRKSLFLDLLQKQEARLTLAAGLTQARREPPAGPAPASLHEVSRLVLDPLQDACRG 480
DB 421 SVSRKSLFLDLLQKQEARLTLAAGLTQARREPPAGPAPASLHEVSRLVLDPLQDACRG 480
QY 481 FYQDGRFGDRRRAKGPAPKPTGQKMLDLNOKSENPRDLFLMAVILONREHMAITYFAM 540
DB 481 FYQDGRFGDRRRAKGPAPKPTGQKMLDLNOKSENPRDLFLMAVILONREHMAITYFAM 540
QY 541 GQEGVAAALAAKCKILKEMSHLETAEBARATREAKYERLAL----DLFSECVNSERA 595
DB 541 GQEGVAAALAAKCKILKEMSHLETAEBARATREAKYERLAL----DLFSECVNSERA 595
QY 596 FALIVRRNRKWSKTTCHLATEADAKAFPAHDYQAFITRIMWGDMAAGTITLGLGAF 655
DB 601 FALIVRRNRKWSKTTCHLATE-DAKAFPAHDYQAFITRIMWGDMAAGTITLGLGAF 659
QY 656 CFALVYTNLITFSEAPLRTGLDLODLSLDTKSPILYQSGSVBELVEAPRAQGRGP 715
DB 660 CPALVYTNLITFSEAPLRTGLDLODLSLDTKSPILYQSGSVBELVEAPRAQGRGP 719
QY 716 RAVELLTRMRKFWGAPVTVFIGNVVMYFAFLFTYVLLVDFRPPQSGPSEVTLYFW 775

DB 720 RAVELLTRMRKFWGAPVTVFIGNVVMYFAFLFTYVLLVDFRPPQSGPSEVTLYFW 779
QY 776 FTVLVEIRSGFFPDEDTHTLVKFKTLVGNMNMCDWVALFLFVGTGCRMLPSAFEGR 835
DB 780 FTVLVEIRSGFFPDEDTHTLVKFKTLVGNMNMCDWVALFLFVGTGCRMLPSAFEGR 839
QY 836 TVLAMDPMVFTLRILHIFAIHKQGPRIIVERMKNQVFFFLFSLVWLVAVGTTOALL 895
DB 840 TVLAMDPMVFTLRILHIFAIHKQGPRIIVERMKNQVFFFLFSLVWLVAVGTTOALL 899
QY 896 HPHDGRLEWIFRRVLYRPYLIQFQIPLDEIDEARVNCSTHPLLEDSPCPSLIYANVL 955
DB 900 HPHDGRLEWIFRRVLYRPYLIQFQIPLDEIDEARVNCSTHPLLEDSPCPSLIYANVL 959
QY 956 ILLVTEFLVNTVNLMLLAMSFTYQVQVGNATMVKORVLIYEHPRPALAPEI 1015
DB 960 ILLVTEFLVNTVNLMLLAMSFTYQVQVGNATMVKORVLIYEHPRPALAPEI 1019
QY 1016 LLSHLSTLRRVFKEA-----EHRHLERLPPLDQKVTWTWQKENFLSK 1065
DB 1020 LLSHLSTLRRVFKEAHEHREHLEHREHLEHLEHLEHLEHLEHLEHLEHLEHLEH 1079
QY 1066 MEKRRDSEGEVLKRTARVDFAKYGLREDEKRIKLESQINYCSVLVSVADYLAQ 1125
DB 1080 MEKRRDSEGEVLKRTARVDFAKYGLREDEKRIKLESQINYCSVLVSVADYLAQ 1139
QY 1126 GGGPRSSQHCESQVLAADHGGIDGDEQPGAGQPPSDT 1165
DB 1140 GGGPRSSQHCESQVLAADHGGIDGDEQPGAGQPPSDT 1179

RESULT 5

AAB86164 standard; Protein; 1158 AA.

AAB86164;

09-AUG-2001 (first entry)

Mouse MTR1 protein.

MTR1; TRP-related protein; Ca2+ regulation; calcium regulation; tumor; transient receptor potential family; BMS; Beckwith-Wiedemann syndrome; 11p15.5 abnormality; chromosome 11; anticancer; developmental activity; intracellular calcium ion regulation; hormone; growth factor; apoptosis; cell growth; cell death; cell differentiation; urogenital disease; polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor; rhabdomyosarcoma.

Mus sp.

W0200132693-A2.

10-MAY-2001.

06-NOV-2000; 2000MO-DE03876.

04-NOV-1999; 99DE-1053167.

(UVGU-) UNIV GUTENBERG JOHANNES.

Prawitt D, Pelletier J, Zabel B;

WPI; 2001-316417/33.

N-PSDB; AAH20623.

DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann

syndrome and tumor, also related proteins and antibodies -

Disclosure, Fig 11; 46pp; German.

This invention describes a novel DNA sequence (i) encoding the MTR1

protein that: (i) has at least one biological activity of a TRP
 CC (transient receptor potential) family protein; (ii) is connected with
 CC etiology of BMS (Beckwith-Wiedemann syndrome) and/or (iii) is connected
 CC with tumors involving 11p15.5 abnormalities. The products of the
 CC invention have anticancer and developmental activity. MRI is involved in
 CC regulation of intracellular calcium ion levels, which are essential for
 CC cellular responses to hormones and/or growth factors; also in apoptosis
 CC and cell growth, death and differentiation, and in urgent diseases,
 CC including polycystic kidney disease. (I) and related ribozymes, antisense
 CC RNA, proteins and antibodies (Ab) are used to treat or prevent diseases
 CC associated with altered expression of the MRI gene or activity of its
 CC protein, or with calcium influx into cells, e.g. BMS, Wilms tumor,
 CC rhabdoid tumors and rhabdomyosarcoma. Probes from (I), or Ab, are also
 CC used for diagnosis of such diseases. (I) can also be used for recombinant
 CC production of MRI proteins (II) (used for analysis, characterization and
 CC therapy), as tissue or chromosomal markers, for identifying genetic
 CC diseases and related sequences, as primers for genetic fingerprinting, as
 CC source of oligonucleotides for biochips, and to raise anti-protein or
 CC anti-DNA antibodies. (II) are used to raise Ab, as reagents in
 CC competitive assays for (II), as tissue markers; for identifying
 CC interacting proteins and in screening for (anti)agonists. This sequence
 CC represents the murine MRI gene described in the method of the invention.
 XX

Sequence 1158 AA;

Query Match 83.2%; Score 5068.5; DB 22; Length 1158;

Best Local Similarity 83.9%; Pred. No. 0;

Matches 980; Conservative 66; Mismatches 109; Indels 13; Gaps 4;

1 MODVGPSPGPDADRRELGLHGEVNFSGSKKRGFVVPSPGAVSLFDLLAEM 60
 1 MOTTGSSCGSPPTDGEWEPILCRGEINFGSGKKRGKGFVVPSPAVSVLPELLTEM 60
 61 HLPAPNLVSLVEEOPFPMKSWLRLKGLYKAAQSTGAMITLSALVGLARHQAV 120
 61 HLPAPNLVSLVEEOPFPMKSWLRLKGLYKAAQSTGAMITLSALVGLARHQAV 120
 61 HLPAPNLVSLVEEOPFPMKSWLRLKGLYKAAQSTGAMITLSALVGLARHQAV 120
 121 RHSLASTSTKYRVVAVGMAASLGRVLRHRLLE--EAQEPFPHYPPEDGSGPLCSLDS 178
 121 RHSLASTSTKYRVVAVGMAASLGRVLRHRLLE--EAQEPFPHYPPEDGSGPLCSLDS 178
 121 RHSLASTSTKYRVVAVGMAASLGRVLRHRLLE--EAQEPFPHYPPEDGSGPLCSLDS 180
 179 NLSHFLVPEPPGPKG-DGLTELRLRLLEKHSIQRAGVGGTSGIIEIPVLCVNGDPNTL 237
 181 NLSHFLVPEPPGPKG-DGLTELRLRLLEKHSIQRAGVGGTSGIIEIPVLCVNGDPNTL 240
 238 ERSRAVEQAAPWLLVSGSGIADVLAAVLPQPHLLVPKAEKQEKPKSKHFSMEDIV 297
 241 ERSRAVEQAAPWLLVSGSGIADVLAAVLPQPHLLVPKAEKQEKPKSKHFSMEDIV 300
 298 RMTKLQNTSHOHLTVDFEPEGSEELDTVLKALVACKSHSQEPDYLDELALAVA 357
 301 HMTKLQNTSHOHLTVDFEPEGSEELDTVLKALVACKSHSQEPDYLDELALAVA 360
 358 WDRVDIAKSEIFNGDVEMKSCDLEVMVDALVSNKEPFRVLFYDNGADVADFLTYGRLOE 417
 361 WDRVDIAKSEIFNGDVEMKSCDLEVMVDALVSNKEPFRVLFYDNGADVADFLTYGRLOE 420
 418 LTRSVSRKSLFLPLLRKOEBAFLTLAAGTQOAREPPAPPSFSLHEVSRVLKDTLQDA 477
 421 LYSVSPKSLFLPLLRKOEBAFLTLAAGTQOAREPPAPPSFSLHEVSRVLKDTLQDA 480
 478 CNGFYODGRGRRRAEKGPAPKPTGOKMLLDNOKSENWRRLFLMAVLYONHMAATF 537
 481 CNGFYODGRGRRRAEKGPAPKPTGOKMLLDNOKSENWRRLFLMAVLYONHMAATF 536
 538 WAMGEGVAAALACKILKEMSHLETAEARAATREAKYERLALDIFSECSYNSSEARAFA 597
 537 WAMGEGVAAALACKILKEMSHLETAEARAATREAKYERLALDIFSECSYNSSEARAFA 596
 598 LTVRRNRCSKTTCLHLATEADAKAFPAHDGVAFLTRVWGMMAAGTPILRLGAFPC 657
 597 LTVRRNRCSKTTCLHLATEADAKAFPAHDGVAFLTRVWGMMAAGTPILRLGAFPC 656

658 ALVNTLITFEEBAFLRTGLEDLQDLSLDTESKSPYLQSGRVBELVEAPRAQGRGPR 717
 657 ALVNTLITFEEBAFLRTGLEDLQDLSLDTESKSPYLQSGRVBELVEAPRAQGRGPR 716
 718 VPLLTRMKKEMGAPVTFVGNVVMFAFLFTYVLLVDFRPPPOGSGEPVTLFWVFT 777
 717 AFLTRMKKEMGAPVTFVGNVVMFAFLFTYVLLVDFRPPPOGSGEPVTLFWVFT 776
 778 LVLEIRGCFPTDEDTHLVKKFTLVYGNMKNKCDVAFLEFVGTGCMPLSPAFAGRTV 837
 777 LVLEIRGCFPTDEDTHLVKKFTLVYGNMKNKCDVAFLEFVGTGCMPLSPAFAGRTV 836
 837 LAMFVMTLRLIHFAHKGKPIIVERMKDVFPEFLFSLVLAAYGVTQALLHP 897
 837 LAMFVMTLRLIHFAHKGKPIIVERMKDVFPEFLFSLVLAAYGVTQALLHP 896
 898 HDGRLEWIFRRVLYRPIYQIRGQIPLDEIDARVNCSTHPLLEBSBSCPSLYANWLYL 957
 897 HDGRLEWIFRRVLYRPIYQIRGQIPLDEIDARVNCSTHPLLEBSBSCPSLYANWLYL 956
 958 LTVFLVTVNLVNLMLLTFMFSYTFQVQGNATMFKFORVNLIVEYHERPALAPFTLL 1017
 957 LTVFLVTVNLVNLMLLTFMFSYTFQVQGNATMFKFORVNLIVEYHERPALAPFTLL 1016
 1018 SHLSLTLRRVFKKEAHRKREHLERDLPDLDQKVVTWETVOKENFLSKMKRRDSEGEV 1077
 1017 SHLSLTLRRVFKKEAHRKREHLERDLPDLDQKVVTWETVOKENFLSKMKRRDSEGEV 1076
 1078 LRTKHARVDFIAKYIGIRBQEKRIKCLIESQINTYSVLVSYADVLAAGGGRSSQHC 1137
 1077 LRTKHARVDFIAKYIGIRBQEKRIKCLIESQINTYSVLVSYADVLAAGGGRSSQHC 1136
 1138 GSOLVAADHRGIDGMEQAGAGOPSPDT 1165
 1137 RSOPASARD-----EYLSGLPPSDT 1158

RESULT 6
 ABB83854
 ID ABB83854 standard. Protein; 1158 AA.
 XX
 AC ABB83854;
 DT 30-SEP-2002 (first entry)
 XX
 DE Mouse ltrpc5 SEQ ID NO 5.
 XX
 KW Mouse; ltrpc5; taste; cell signalling; TC-ICS; food; pharmaceutical;
 KW taste cell-specific ion channel subunit.
 XX
 OS Mus sp.
 XX
 PN WO200254069-A1.
 XX
 PD 11-JUL-2002.
 XX
 PF 26-DEC-2001; 2001WO-US49808.
 XX
 PR 29-DEC-2000; 2000US-259379P.
 PR 21-DEC-2001; 2001US-0026188.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Zuker CS, Zhang Y;
 XX
 DR WPI; 2002-583632/62.
 DR N-PSDB; ABB85734.
 XX
 PT Identifying modulators of taste signaling in taste cells for use in
 PT food and pharmaceutical industries to customize and regulate taste, by
 PT determining effect of the compound on a taste cell-specific ion channel
 PT subunit -

PS Claim 1; Page 211; 306pp; English.

XX The invention relates to identifying (M1) a compound that modulates taste
CC signaling in taste cells, by contacting the compound with a eukaryotic
CC host cell or cell membrane which expresses a taste cell-specific ion
CC channel subunit (TIC-1CS), and determining a functional effect of the
CC compound upon a transmembrane ion flux of a predetermined ion.
CC Identifying a compound that modulates taste signaling in taste cells.
CC (M1) is useful for identifying a compound that modulates taste signaling
CC in taste cells, for identifying a compound that binds to a taste cell
CC specific ion channel subunit and for modulating taste signaling in taste
CC cells of a mammal, in particular a human. Modulators identified by (M1)
CC are used by the food and pharmaceutical industries to customize taste,
CC e.g. as additives to food or medicine so that the food or medicine tastes
CC different to the subject who ingests it. Bitter medicines can be made to
CC taste less bitter and sweet substance can be enhanced. The modulators are
CC useful for pharmacological and genetic modulation of taste signaling
CC pathways. The taste modulators can be directly administered to mammalian
CC subjects for modulation of taste in vivo. The present sequence is that of
CC the predicted mouse Itprcs protein of the invention.

XX Sequence 1158 AA;

Query Match 83.2%; Score 5068.5; DB 23; Length 1158;
Beet Local Similarity 83.9%; Pred. No. 0;
Matches 980; Conservative 66; Mismatches 109; Indels 13; Gaps 4;

QY 1 MODVGGPPSPGPDREDELHGEVNFSGGKKGKGFVVPVSGVAPSVLFDLLLEW 60
DB 1 MOTTOSCGPSPDREDEMEPLCGEINFGSGKKGKGFVVPVSGVAPSVLFDLLLEW 60
QY 61 HLPAPNLVSLVGEBOFPAMKSWLRLVRLKGLVKAOSTGAMILTSALRVGLARRVQAV 120
DB 61 HLPAPNLVSLVGEBOFPAMKSWLRLVRLKGLVKAOSTGAMILTSALRVGLARRVQAV 120
QY 121 RDHSLASTSTKRVVAVGMAISLGRVLRRLIE--EAQEDPVHYHEDDGGSGGPICSIDS 178
DB 121 RDHSLASTSTKRVVAVGMAISLGRVLRRLIE--EAQEDPVHYHEDDGGSGGPICSIDS 178
QY 121 RDHSLASTSTKRVVAVGMAISLGRVLRRLIE--EAQEDPVHYHEDDGGSGGPICSIDS 178
DB 121 RDHSLASTSTKRVVAVGMAISLGRVLRRLIE--EAQEDPVHYHEDDGGSGGPICSIDS 178
QY 179 NLSHFILVEPPGPKG-DGLTELRLLEKHSSEORAGVGGSGSIEIPVLCILVNDPMTL 237
DB 181 NLSHFILVEPPGPKG-DGLTELRLLEKHSSEORAGVGGSGSIEIPVLCILVNDPMTL 237
QY 238 ERISRAVEQAAPWLLVSGSGIADVALVNOQPHLLVKEVAKQEKPEKPFSEKMFEDI 297
DB 241 ERISRAVEQAAPWLLVSGSGIADVALVNOQPHLLVKEVAKQEKPEKPFSEKMFEDI 297
QY 298 RWTKLQNTSHQHLTYDFEQQSGSELDVYILKALYKACKSHQSEPODYLDLKLAVA 357
DB 301 HMTLQNTSHQHLTYDFEQQSGSELDVYILKALYKACKSHQSEPODYLDLKLAVA 357
QY 358 WDRVDAIASEIFNGQVEWKSGLDEVMVDALVSNKPEEVRLLFVNDGAVVADPFLTYGRLOE 417
DB 361 WDRVDAIASEIFNGQVEWKSGLDEVMVDALVSNKPEEVRLLFVNDGAVVADPFLTYGRLOE 417
QY 418 LYSRVSRSKSLFDLQKQSEARLLTAGLQTOAREPAPGPAFSLHEVSRYLKDPLQDA 477
DB 421 LYSRVSRSKSLFDLQKQSEARLLTAGLQTOAREPAPGPAFSLHEVSRYLKDPLQDA 477
QY 478 CRGFYQDGRPDGRRRAEKGPAKPTGQKLLDLNOKSENPMRDLFLMAVLQNRHEMATYF 537
DB 481 CRGFYQDGRPDGRRRAEKGPAKPTGQKLLDLNOKSENPMRDLFLMAVLQNRHEMATYF 537
QY 538 WAMGOEGVAALAAACKILKEMSHLETEAARATREAYEELADLFSECSNSGARFA 597
DB 537 WAMGOEGVAALAAACKILKEMSHLEKEAVARWMEAYEELADLFSECSNSGARFA 596
QY 598 LLYRRNRCKSKTTCILHLEADAKAFPAHDGVOAFLTRIMGMMAAGPPIRLIGAPLCP 657
DB 597 LLYRRNRCKSKTTCILHLEADAKAFPAHDGVOAFLTRIMGMMAAGPPIRLIGAPLCP 656
QY 658 ALVTNLTITSEEARPLRTGLEDLQDLSDLTEKSPLYLQSRVEELVAPPAQDGRGPA 717
DB 658 ALVTNLTITSEEARPLRTGLEDLQDLSDLTEKSPLYLQSRVEELVAPPAQDGRGPA 717

DB 657 ALIYTNLTISFSEDAPQRMDLEDLOEPDSLDNEKSFCSRGQLEKLTAPRAPGLGPOA 716
QY 718 VFLTRMRKFWGAPVTVFLGVNVMWFAPLFTFTVLLVDPFRPPGSPGSEVTLVFWFT 777
DB 717 AFLTRMRKFWGAPVTVFLGVNVMWFAPLFTFTVLLVDPFRPPGSPGSEVTLVFWFT 776
QY 778 LYLBEIRGFPFTDEBTHLYKKFTLYVGDNNKCDMVAFLPIVGTCTMLPSAFBAGRTV 837
DB 777 LYLBEIRGFPFTDEBTHLYKKFTLYVGDNNKCDMVAFLPIVGTCTMLPSAFBAGRTV 836
QY 838 LAMPVNTVLLIHFALHKKQGLKILYVENMKDVFPLFLPSWLVAVYTTQALLHP 897
DB 837 LAIFEMFTLLIHFALHKKQGLKILYVENMKDVFPLFLPSWLVAVYTTQALLHP 896
QY 898 HDGRLEWTFRVLVRLPYQIRGOIPLDEIDARVNCSTHPLLEDSPECPSLYANWLYL 957
DB 897 HDGRLEWTFRVLVRLPYQIRGOIPLDEIDARVNCSTHPLLEDSPECPSLYANWLYL 956
QY 958 LVTFLVTVNLLNMLLAMSSTFQVQVGNATVFWKFORVNLIVYHERPALAPFTLL 1017
DB 957 LVTFLVTVNLLNMLLAMSSTFQVQVGNATVFWKFORVNLIVYHERPALAPFTLL 1016
QY 1018 SHLSLTLRRVFKKAHEKREHLERDLPPLDQKVYMETVOKENFLSMERRRDSEGEV 1077
DB 1017 SHLSLTLRRVFKKAHEKREHLERDLPPLDQKVYMETVOKENFLSMERRRDSEGEV 1076
QY 1078 LRKTAHRYDPIAKYLGRLREGEKIKLESQINVCVSVSVAVYLQCGGPRSSQHGE 1137
DB 1077 LRKTAHRYDPIAKYLGRLREGEKIKLESQINVCVSVSVAVYLQCGGPRSSQHGE 1136
QY 1138 GSOLVADHRGIDGWEOPGAGOPPST 1165
DB 1137 RSQPASARDR-----EYLSGLPSPDT 1158

RESULT 7

AAB86166 ID AAB86166 standard; Protein; 1158 AA.

AC AAB86166;

DT 09-AUG-2001 (first entry)

XX Mouse MTR1 protein #2.

XX MTR1, TRP-related protein; β 2+ regulation; calcium regulation; tumor;
XX transient receptor potential family; BMS; Beckwith-Wiedemann syndrome;
XX 11p15.5 abnormality; chromosome 11; anticancer; developmental activity;
XX intracellular calcium ion regulation; hormone; growth factor; apoptosis;
XX cell growth; cell death; cell differentiation; urogenital disease;
XX polycystic kidney disease; calcium influx; Wilms tumor; rhabdoid tumor;
XX rhabdomyosarcoma.

XX Mus sp.

XX WO200132693-A2.

XX 10-MAY-2001.

XX 06-NOV-2000; 2000WO-DE03876.

XX 04-NOV-1999; 99DE-1053167.

XX (UYGU-) UNIV GUTENBERG JOHANNES.

XX Prawlit D, Pelletier J, Zabel B;

XX WPI; 2001-316417/33.

XX DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann
XX syndrome and tumors, also related proteins and antibodies -

XX Disclosure; Fig 12; 46pp; German.

QY 598 LVRNRCSKTTCLHLATBADAKAFFAHGVOAFLTRIWWGDMAGTPILRLGAF LCF 657

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DR N-PSDB; AA199707.
 XX A new transient receptor potential channel, designated TRP8, is
 PT expressed in taste receptor cells and associated with perception of
 PT bitter and sweet taste, and is useful to find new flavour enhancers
 XX
 PS Claim 8; Fig 2; 55pp; English.
 CC The invention relates to a mouse and human transient receptor potential
 CC channel, TRP8, expressed in taste receptor cells and associated with the
 CC perception of bitter and sweet taste. Modulators of TRP8 are useful as
 CC flavour enhancers in foods, beverages and pharmaceuticals.
 XX
 SQ Sequence 1157 AA;
 Query Match 83.0%; Score 5053; DB 23; Length 1157;
 Best Local Similarity 83.8%; Pred. No. 0;
 Matches 979; Conservative 66; Mismatches 109; Indels 14; Gaps 5;
 QY 1 MODVGGPPGSPGDAEDRRELGLHGEVNFSGSGKRGKRVNPSGVAHSVLFDDLLEW 60
 DB 1 MOTTQSSCPGSPPTDEDMEPILCRGEINFGSGKRGKRVNPSVAFELLLEW 60
 QY 61 HLPAPNLVSVLGEERPFAMKSKMLDVLRKGLVKAAOSTGAMILTSARVGLARVQAV 120
 DB 61 HLPAPNLVSVLGEERPFAMKSKMLDVLRKGLVKAAOSTGAMILTSARVGLARVQAV 120
 QY 121 RDHSLASTSTKRVVAVAGMASLGRVLRHRIIE--BAODEPVHYEPEDDGSQGPLCSLDS 178
 DB 121 RDHSLASTSTKRVVAVAGMASLGRVLRHRIIE--BAODEPVHYEPEDDGSQGPLCSLDS 180
 QY 179 NLSHFIVEPPEPGKG-DGTELRLRLERKHISEGAGYGGTGSIRIPVLCILVNDPNTL 237
 DB 181 NLSHFIVEPPEPGKG-DGTELRLRLERKHISEGAGYGGTGSIRIPVLCILVNDPNTL 240
 QY 238 ERISRAVQOAPWMLIVNGSGGIADVLALVNOPHLLVVKVAEKOKERKPEKPEMDIV 297
 DB 241 ERISRAVQOAPWMLIVNGSGGIADVLALVNOPHLLVVKVAEKOKERKPEKPEMDIV 300
 QY 298 RMTKLQVITSHOHLTYVDFEFGESSELDVYILKALVKACSHSQEPDYLDELKLVAV 357
 DB 301 RMTKLQVITSHOHLTYVDFEFGESSELDVYILKALVKACSHSQEPDYLDELKLVAV 360
 QY 358 WDRVDIAKSEIFNGDVNWKSCDLEEVNDALVSNKPEVRLFVDNADVADFLTYGRLOE 417
 DB 361 WDRVDIAKSEIFNGDVNWKSCDLEEVNDALVSNKPEVRLFVDNADVADFLTYGRLOE 420
 QY 418 LYRSVSRKSLFDLLQKQOEARKLTLAGLGTQOAEPPAGPAPFSLHESRYLKDLODA 477
 DB 421 LYHSVSPKSLFELLQKQHEBGRRLTAGLGAQOARELPGLPAFSLH-VSRVLKDFLHDA 479
 QY 478 CRGFQODRPGDRRAEKGPAKRPYGOKMLDLNOKSENPMRDLFLMVLNQRHMAIYF 537
 DB 480 CRGFQODRPGDRRAEKGPAKRPYGOKMLDLNOKSENPMRDLFLMVLNQRHMAIYF 535
 QY 538 WAMGEGVAAALAAACKILKEMSHLETEAARATREAKYERLADLFSECYNSNBARAFA 597
 DB 536 WAMGEGVAAALAAACKILKEMSHLEKEAEVARTMEATYEQALDLFSECYNSNBARAFA 595
 QY 598 LLVRNRKWSKTTCTHATLATEADAKAFPAHDGQVAFULRIWGDMAAGTPILRLGAPL 657
 DB 596 LLVRNRKWSKTTCTHATLATEADAKAFPAHDGQVAFULRIWGDMAAGTPILRLGAPL 655
 QY 658 ALVVTNLITFSEBAPLRTGLDLODLSDLTEKSLYLQGSNVEVLVAPRAGQGRGPR 717
 DB 656 ALVVTNLITFSEBAPLRTGLDLODLSDLTEKSLYLQGSNVEVLVAPRAGQGRGPR 715
 QY 718 VFLLTRMRKFGAPVFLGNVVMYFAFLFTVYLVDFRPPPGSPGSEVTLVFWFT 777
 DB 716 AFLFLTRMRKFGAPVFLGNVVMYFAFLFTVYLVDFRPPPGSPGSEVTLVFWFT 775
 QY 778 LVLEIRGCFPTDEDTLHKKFTLYVGNWNAKCMVAIFLPIVGTCTMMLPSAFAAGTIV 837

DB 776 LVLEIRGCFPTDEDTLHKKFTLYVGNWNAKCMVAIFLPIVGTCTMMLPSAFAAGTIV 835
 QY 838 LAMDFMVTTLRLIIFAIHKOLGPKIIVERMMKDVFFFLFSYMLVAVGTTQALLHP 897
 DB 836 LAIDFMVTTLRLIIFAIHKOLGPKIIVERMMKDVFFFLFSYMLVAVGTTQALLHP 895
 QY 898 HDGRLEWIFRRVLYRPIYQIIGQIPLDEIDARVNCSTHPLLEDSPSCPSLYANWVYL 957
 DB 896 HDGRLEWIFRRVLYRPIYQIIGQIPLDEIDARVNCSTHPLLEDSPSCPSLYANWVYL 955
 QY 958 LLVTFLLVTNVLNMLNLIAMSYFOVVGAAATMFKORVNLIVYERBALAPPILL 1017
 DB 956 LLVTFLLVTNVLNMLNLIAMSYFOVVGAAATMFKORVNLIVYERBALAPPILL 1015
 QY 1018 SHLSLTLRVPKAEHREHLERDLPDLPDOKVYMETVYOKENFLSKERRRDSGEV 1077
 DB 1016 SHLSLTLRVPKAEHREHLERDLPDLPDOKVYMETVYOKENFLSKERRRDSGEV 1075
 QY 1078 LRKTAHRVDLFAKYLGLRQEKRIKCLSQINYSVLSSVADVLAAQGGPRSSQHC 1137
 DB 1076 LRKTAHRVDLFAKYLGLRQEKRIKCLSQINYSVLSSVADVLAAQGGPRSSQHC 1135
 QY 1138 GSQVLAADHRCGIDGWEQPGAGOPPSDT 1165
 DB 1136 RSQPASARD-----EYLSGLPPSDT 1157
 RESULT 9
 ID ABB83853
 AC ABB83853 standard; Protein, 1164 AA.
 XX ABB83853;
 DT 30-SEP-2002 (first entry)
 XX
 DE Rat L-TRP SEQ ID NO 2.
 XX
 KM Rat; L-TRP; taste; cell signalling; TC-ICS; food; pharmaceutical;
 XX taste cell-specific ion channel subunit.
 OS Rattus sp.
 XX
 PN MO200254069-A1.
 PD 11-JUL-2002.
 XX
 PF 26-DEC-2001; 2001MO-US49808.
 XX
 PR 29-DEC-2000; 2000US-259379P.
 PR 21-DEC-2001; 2001US-0026188.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Zuker CS, Zhang Y;
 XX
 DR WPI; 2002-583632/62.
 XX
 PT N-PSDB; ABB85732.
 PT
 CC Identifying modulators of taste signalling in taste cells for use in
 CC food and pharmaceutical industries to customize and regulate taste, by
 CC determining effect of the compound on a taste cell-specific ion channel
 CC subunit -
 CC
 CC Claim 1; Page 63; 306pp; English.
 CC
 CC The invention relates to identifying (MI) a compound that modulates taste
 CC signalling in taste cells, by contacting the compound with a eukaryotic
 CC host cell or cell membrane which expresses a taste cell-specific ion
 CC channel subunit (TC-ICS), and determining a functional effect of the
 CC compound upon a transmembrane ion flux of a predetermined ion,
 CC identifying a compound that modulates taste signalling in taste cells,
 CC (MI) is useful for identifying a compound that modulates taste signalling
 CC in taste cells, for identifying a compound that binds to a taste cell

specific ion channel subunit and for modulating taste signaling in taste cells of a mammal. In particular a human. Modulators identified by (M1) are used by the food and pharmaceutical industries to customize taste, e.g. as additives to food or medicine so that the food or medicine tastes different to the subject who ingests it. Bitter medicines can be made to taste less bitter and sweet substance can be enhanced. The modulators are useful for pharmacological and genetic modulation of taste signaling pathways. The taste modulators can be directly administered to mammalian subjects for modulation of taste in vivo. The present sequence is that of the rat L-TRP protein of the invention.

Sequence 1164 AA;

Query Match 81.9%; Score 4988.5; DB 23; Length 1164;
Best Local Similarity 82.6%; Pred. No. 0;
Matches 963; Conservative 76; Mismatches 116; Indels 11; Gaps 3;

1 MODVGPSPGSGPDADRRRLGLHGEVNFVGGSGKKRGKRVNPGSAPVLFDLIAEM 60
9 MEMAOSGSGSPPTDGDGHEPVLCKGEVNFVGGSGKKRSKFVNPVSNVSMLEFILLTEM 68
61 HLPAPNLVSVLVEEQPFAMKSWLRDLVKGLVKAQSTGAMILTSALRVGLARHVGQAV 120
69 HLPAPNLVSVLVEERLFAMKSWLRDLVKGLVKAQSTGAMILTSALRVGLARHVGQAV 128
121 RHSLASTSTKRVYAVGMAISGRVLRHRIIEAQPDPVNYPEDDGSQGLCSLSNLT 180
129 RHSLASTSTKRVYAVGMAISGRVLRHRIIEAQPDPVNYPEDDGSQGLCSLSNLT 188
181 SHFIVEPSPGSG-DGLTELRLLEKHSIQRAGYGGTSGIPIVLCILVNGDPVTLER 239
189 SHFIVEPSPGSG-DGLTELRLLEKHSIQRAGYGGTSGIPIVLCILVNGDPVTLER 248
240 ISRAVEQAAPMLILVGGSGIADVLAAVNPQPHLVKVAEKQPKFEPSEKHSFWSMEDIVN 299
249 MSRAVEQAAPMLILVGGSGIADVLAAVNPQPHLVKVAEKQPKFEPSEKHSFWSMEDIVN 308
300 TLLNITSHOHLITVYDEFGSGSEEDLVITLKAIVKAKSHSOEPQDYLDELKLAIVAMD 359
309 TLLNITSHOHLITVYDEFGSGSEEDLVITLKAIVKAKSHSOEPQDYLDELKLAIVAMD 368
360 RVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKPEFVRLVFDNGADVADFLTYRLOELY 419
369 RVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKPEFVRLVFDNGADVADFLTYRLOELY 428
420 RSVSRKSLIFDLIQKQEBARLTLAGLGTQQAEPAPGAPASLHVSRYLKDFLODADR 479
429 HSVSPKSLIFELLERKHEGRLLTAGLGAQOTRKLPGVGLPASFHVSRYLKDFLODADR 488
480 GFYQDGRPDRRRAEKAPKPTGQKMLDLNOKSENPMRDLFLMAVLGNRHMAITYMA 539
489 GFYQDGRPDRRRAEKAPKPTGQKMLDLNOKSENPMRDLFLMAVLGNRHMAITYMA 544
540 MGOEGVAAALAACTIKEMSHLETEAARATREAKYERLADLFSECYNSSEARAFALL 599
545 MREGVAAALAACTIKEMSHLEKEAEVARTREAKYERLADLFSECYNSSEARAFALL 604
600 VRRNRCSYTTCTHILATEADAKAFPAHDGVQAFETIRIMGDMAGTPIIRLLGAFICPAL 659
605 VRRNRCSYTTCTHILATEADAKAFPAHDGVQAFETIRIMGDMAGTPIIRLLGAFICPAL 664
660 VTNLTITSEEARLRTGLDLDLSDLPDEKSPYLGLQSRVELVAPAAQDGRGRAPV 719
665 IYTNLTITSEEARLRTGLDLDLSDLPDEKSPYLGLQSRVELVAPAAQDGRGRAPV 724
720 LITRMRKFGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPPGSGPEVTLTFWFTV 779
725 LITRMRKFGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPPGSGPEVTLTFWFTV 784
780 LEEIRGGFTDEDTHLVKFTLVYVGNMKNCDMAVIFLFTVGTGCMLEPSAFAGRTVLA 839
785 LEEIRGGFTDEDTHLVKFTLVYVGNMKNCDMAVIFLFTVGTGCMLEPSAFAGRTVLA 844

QY 840 MDEFVETRLIHIFAIHKQLGPKIIVVERMKKDVFFFLFPLSVMLVAVGTTQALLAPHD 899
DB 845 IDFWFTLRLLHIFAIHKQLGPKIIVVERMKKDVFFFLFPLSVMLVAVGTTQALLAPHD 904
QY 900 GRLEWIFRRVLYRPLQIFGOIPLDEIDEARVNSTHLLLEDSPSCSYANMVLITLL 959
DB 905 GRLEWIFRRVLYRPLQIFGOIPLDEIDEARVNSTHLLLEDSPSCSYANMVLITLL 964
QY 960 VTFLLVTNVLMLNLIAFSTFTFOVQGNADMFKFOYHLIVHGRPALAPPTILLSH 1019
DB 965 VTFLLVTNVLMLNLIAFSTFTFOVQGNADMFKFOYHLIVHGRPALAPPTILLSH 1024
QY 1020 LSLTRRVFKKBAEKREHLERDLPDLOKRVMTWETVQKENFLSKMEKRRDSGEVLR 1079
DB 1025 LSLVAKQVFRKDAQKHQHLERDLPDLOKRVMTWETVQKENFLSKMEKRRDSGEVLR 1084
QY 1080 KTAHRVDIATYKIGLREQEKRIKLEQINVCYLVSVADVLAQGGSPSSQCGEGS 1139
DB 1085 KTAHRVDIATYKIGLREQEKRIKLEQINVCYLVSVADVLAQGGSPSSQCGEGS 1144
QY 1140 QLVADHRGGIDGMEQPGAGPPSPT 1165
DB 1145 QPASADR-----EYLAAGLPHSDT 1164

RESULT 10

AA86163 standard; Protein; 872 AA.

AA86163;

09-AUG-2001 (first entry)

Human MTR1 protein without exon 18 fragment.

MTR1, TRP-related protein; Ca²⁺ regulation; calcium regulation; tumor; transient receptor potential family; BWS; Beckwith-Wiedemann syndrome; 11p15.5 abnormality; chromosome 11; anticancer; developmental activity; intracellular calcium ion regulation; hormone; growth factor; apoptosis; cell growth; cell death; cell differentiation; urogenital disease; kidney polydysplasia; kidney disease; calcium influx; Wilms tumor; thaboid tumor; thaboidoma; carcinoma.

Homo sapiens.

WO200132693-A2.

10-MAY-2001.

06-NOV-2000; 2000WO-DE03876.

04-NOV-1999; 99DE-1053167.

(UYGU-) UNIV GUTENBERG JOHANNES.

Prawitt D, Pelletier J, Zabel B;

WPI, 2001-216417/33.

N-PSDB; AAH20574.

DNA encoding MTR1 protein, useful e.g. for treating Beckwith-Wiedemann syndrome and tumors, also related proteins and antibodies -

Claim 10; Fig 4; 46pp; German.

This invention describes a novel DNA sequence (1) encoding the MTR1 protein that: (i) has at least one biological activity of a TRP (transient receptor potential) family protein; (ii) is connected with etiology of BWS (Beckwith-Wiedemann syndrome) and/or (iii) is connected with tumors involving 11p15.5 abnormalities. The products of the invention have anticancer and developmental activity. MTR1 is involved in regulation of intracellular calcium ion levels, which are essential for cellular responses to hormones and/or growth factors; also in apoptosis

Query Match 39.9%; Score 2430.5; DB: 23; Length 1166;
 Best Local Similarity 45.4%; Pred. No. 2.1e-221;
 Matches 532; Conservative 177; Mismatches 352; Indels 111; Gaps 26;

26 GEVNGSGGKRGKRVVPVSPVLPFLDLAEVHLPAFNLVSLVGECPFANKSMWR 85
 28 GELDTGACRKSNLRLSDRTDPAVYSLVTRTGAFAPNLVSLVSGSGPVLTQMLQ 87
 86 DVLKGLVKAOSTGAMILTSALRVGLAHVGAQRVDSLASTSTKRVVAVGMSLGRV 145
 88 DLLRGLVAAOSTGAMIVTGLHTGIGHVGVAAVRDHQMASTG-GTKVAVAGVAPWGVV 146

146 LHRRLLEKQEDPPHY-----PEDDGSQGPLCLDLSLHFIIVPEPPKGDVTEL 200
 147 RNRDTLINPKSFPARYRWRGDEP--GVQFP--LDVYSAFVLDDGTGCLGGRNF 201

201 RLLEKHISEQAGYGTGSEIEIPVLCILVNGDPMTLERISRAVEQAPFLLVSGGIA 260
 202 RLRLSEYISQKTVGCTG-IDIPVLLLLIDGDEKMLTLENATQALPCLLVASGGAA 260

261 DVLALVNPPLVLP-----KVAEKQPEKPSKHSFWMEDIVRMTKLLQNTSHQHL 313
 261 DCIAETLED--TLAPSGGARGQGEARDRIIRFFPK-----GDLEVLAQVERIMTRKEL 313

314 TVYDPEQESSELDYIILKLVKACKSHQEPQDYDELKLVAMRDVLIASEIFENGDV 373
 314 TVYSSD-DSSEETIVLALVAC--GSSEASAYIDELRLVAMNRVLIQSELRGDI 370

374 EWKSCDLEEVMDALVSNKPEFVRLFVDNGADVDELTVYGRLOELTVSRYSRSLJFDLQ 433
 371 QMRSPLEASLMDALLNDREPEFRLILSHGLSLHTMRILAQLYSAPNSLIRNLLD 430

434 KROEARLTLAGL--GTQAREPPAGRPAPSLHEVSRVLDKFLQACRGFYODRGPRDR 491
 431 QASHSAGTAPALKGAAELRP-----DVGHVLRMLGKVCARYSYSGGAMDH 480

492 RAEKGAKPRTGKXLLDLNQS-----ENPRDLFIWAVLONRHEMATYFAMQ 542
 481 ----GGGFGESWYLLSDKATSPSLDLGAGLPASDILLWLLNLRQMAVTFEMWS 535

543 EGVAAALACKILKEMSHLETEEAARATREA--KYERLALDLSECYNSSEARAFALV 600
 536 NAVSSALGACILLRWARLEPDEBARAKDLAFKEGCVVDLFGCYSSSEVBARALL 595

601 RNRCSKTTCHLATEADAKAFPAHDGVQAFITRIWGMMAATPILKGAFLCPALV 660
 596 RRCPLMGDATCIQLAMQADARAFADGVQSLTQKMWGMMASTPIWLVAFPCPPLI 655

661 YTNLITF--SEAPLRTGLDLODLSLDTSEKSLVGLQSRVELVAPRAQD----- 712
 656 YTRLITFRKSEETPEELE--FDMSVINGECPGTADPAEKTPIGVPRQSRPGCCG 713

713 --RGPRAVFLITMRKFWGAPVTVLGNVVPAPFLFTYVLLVDFRPPQSPGSEVTV 770
 714 RCGRRG---LRMHFWGAPVITIFMGNVSVYLLFLLFSRVLVDFGPAP--PGLLELL 768

771 LYVWFTLVLEIRQGFTEDETR-----HLVKFTLYVGDNMKCMVAFLPL 819
 769 LYFWAFTLLCEELRQGISGGGSLASGPGPHASLSQRILYIADSMQCDLVALTCFL 828

820 VGTGCMTPSAFEAGRTVLAMDMPVFLRLIHTFAHKGOLGPKTIIVERMKVPPFLP 879
 829 LGVGCRTLPGLYHGRVLCIDIMVFTVRLHITFNKQGGPKIVISKMKKGVFFFLP 888

880 LSVMLVAVGVTQALLPHDGRLEWIFRRLVYRPIYQIFQDIPLDEIDEARV--NCSTH 936
 889 LGMVLVAVGATGLRPRSDPSILRRFYRPIYQIFQDIPEDMDVAMHSNCSSE 948

937 PLLLEDS-----SCPSLVANMLVILLVTFLLVTVNLLNLLIAMSSTFYQVQGNAM 991
 949 PGFWAHPGAGAGTCVAGVYANMLVLLLVIFLLVANILLIAMSSTFYGVQGNDSL 1008

992 FMKFORVNLIVEHERPALAPPFILLSHLSTLRRVFK-----EAEKKEHLERD 1042
 1009 YMKQGRVYLIEFFHSRPLAPPFIVISHLRLLQLCRPRSPQSSPALHFRVYLSKE 1068

1043 LPDLDQKVTWETVQKENFLSKMEKRRRDSGEVLKRTIARVPFIKYLGLAEQEKRI 1102
 1069 ----AERKLTWESVHENFLLARARDREDSRLKTSQVDLALQOLCHIREYQRL 1124

1103 KLESQINVCGLVSVADVLAQG-----GGP 1129
 1125 KLEREVQCCSRVLGVAEALSRLALPPGGP 1156

RESULT 12
 AA95436
 ID AA95436 standard; Protein; 1214 AA.

AA95436;
 10-OCT-2000 (first entry)

Human calcium channel SOC-3/CRAC-2.
 SOC-3/CRAC-2; calcium channel; human; store operated channel;
 calcium release activated channel; therapy; diagnosis;
 lymphocyte proliferative disorder.

Homo sapiens.
 WO20040614-A2.
 13-JUL-2000.

20-DEC-1999; 99WO-US29996.
 30-DEC-1998; 98US-0114220.
 29-JAN-1999; 99US-0120018.
 22-JUN-1999; 99US-0140415.

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
 Scharenberg AM;
 WPI; 2000-465957/40.
 N-PSDB; AAA99923.

New SOC/CRAC calcium channel polynucleotides and polypeptides used to
 diagnose and treat proliferative disorders associated with the channel,
 and to screen for novel modulators of the channel.

Claim 14; Page 100-103; 108pp; English.

The present sequence is that of human SOC-3/CRAC-2, a member of
 a novel family of store operated channel (SOC) or calcium release
 activated channel (CRAC) polypeptides that modulate Ca2+ flux into
 and out of a cell, and which may be activated upon depletion of
 Ca2+ from intracellular calcium stores, allowing Ca2+ influx into
 a cell. SOC-3/CRAC-2 is expressed predominantly in colon and kidney.
 Compositions for expressing functional SOC/CRAC calcium channel
 polypeptides in cells are expected to be useful for treating
 patients that have reduced extracellular calcium influx into their
 SOC/CRAC-expressing cells. They will also be useful for delivering
 therapeutic and/or imaging agents to such cells to modulate
 proliferation and growth. SOC/CRAC polypeptides also represent
 targets for designing and/or identifying inhibitors that block
 lymphocyte proliferation and binding agents that selectively bind
 to SOC/CRAC polypeptides to which drugs or toxins can be conjugated
 for delivery to SOC/CRAC expressing cells. Methods for determining
 the level of SOC/CRAC expression in a subject can be used to assess
 the presence, or absence, or stage of a proliferative disorder,
 e.g. a lymphocyte proliferative disorder.

Sequence 1214 AA;
 SQ

Query Match 39.9%; Score 2430.5; DB 21; Length 1214;
 Best Local Similarity 45.4%; Pred. No. 2.3e-221;
 Matches 532; Conservative 177; Mismatches 352; Indels 111; Gaps 26;

QY 26 GEVNFSGGKRRKGVFVPSGVAPSVLPDLLAEWHLPAPNLVSLVGEOPFAMKSWLR 85
 DB 76 GELDTGAGRKHSNFRSLSDRTDPAAVSLVTRTWGFRAPNLVSVLGGSGGPVLTQWLQ 135
 QY 86 DVLARKGLVAAOSTGAMILTSALRVGLARHVGAVRDSHSLASTSKVRVAVAGMASLGRV 145
 DB 136 DILRRGIVRAAOSTGAMIVTGLHTGIGHVAVARDHMASTG-GTKVAVAGVAPWGVV 194
 QY 146 LHRRIIEEAQEDFPVHY-----PEDDGSQGPLCSLDSNLSHFIIVERPSPGKDGJTEL 200
 DB 195 RNRDILINPKGSFPARYRWGDPED--GVQFP--LDVYSAFVLVDGTHCCLGGENRF 249
 QY 201 RLRLKXHTSEQAGVGTGSIETIPVLCILVNGDPNTLERISAVQAAPMLILVSGGIA 260
 DB 250 RLRLSEYISQKXTGVGTG-IDIPVLLILIDGDEKMLTRIENATQAOLPCLILVAGSGGA 308
 QY 261 DVLAAVLNQPHLLV-----KVAEKQFKEKFPKSHSWEDIVAWTKLQNTSHOHL 313
 DB 309 DCLAEITLED--TLAAGSGGARGGEARDKRRFFPK-----GDLEVLAQOVERIMTRKELL 361
 QY 314 TVYDFEQGSEBELDVIILKALVKACKSHSQBPQDYLDELKLAIVANDRYDAKSEIFNGDV 373
 DB 362 TVYSSB-DGSEBEFTIVLKALVKAC--GSSSEASAVLDELRLAVANNRDIQSELFRDII 418
 QY 374 EWSGDLFEWVADLVSKNKEFVRLFVNGADVADFLTYGRLOELIYRSYRSKSLPDLIQ 433
 DB 419 QMRSHFLASLMDLALNDRPEFVRLILSHGLSHFLTPMRLAQLYSAPNSLIRNLID 478
 QY 434 RKOEBARITLAGL--GTOOAREPPAGPPAFSLHEYSRYLKDFDQACRFYDGRPRR 491
 DB 479 QASHSAGTKAPALKGGAELRPP-----DVGAVLRKMLGMCAPRYPSGAMPBH 528
 QY 492 RAEKGPAPRPTGQKWLIDLNOKS-----ENPRDLFLWAVLONHEMATYFWAMQ 542
 DB 529 -----PGQGFGBSMYLLSDKATSPSLSDAGLQAPMSDULLMALILNQAQWAMYMWEGS 583
 QY 543 EGVAAALAAKILKMSHLETEAARATREA--KYERLADLDEECYSNSEAPAFALLV 600
 DB 584 NAVSSALGACILLRVARLEPDAEAPARRKDLAFEBEGVDLFECEYRSESEVRARILL 643
 QY 601 RRNCWSTKTTCGLHATEADAKAFPAHDGVOAFITRMWGDMAAGPIRLGLAFICPLV 660
 DB 644 RRCPIMGDAITCQLMADARAFPAQDGVQSLITQKMGDMASTPPIVALVLAFFCPPLI 703
 QY 661 YTNLITF--SEBAPLRTGLLEDLQDLSLDTKSPLYGQSRVEELVEAPRAQD----- 712
 DB 704 YTRLITFKSEBEPRELE--FDMDSVINGEGPAGTADPAEKPTLGVPRSGRGCCGG 761
 QY 713 --RBRPAVLLTRRKFWGAPYTVFLGNVVMFAFLFTYVLLVDPFRPPQSGSPSEVT 770
 DB 762 RCGGRRC---RRMFHFWGAPVITFMGNVSYLLFLFLFSHYLLVDFQAPAP--PGSELRL 816
 QY 771 LYPWFVTLVLEIRGCFPTDEDT-----HLVKFTLYVGDMMNKKDMAVILFI 819
 DB 817 LYPFAFTLCEELRGSLSGGGSGLASGPGGSHASLSQRLRYLADSNQCDVALVLTCL 876
 QY 820 VGVTCRMLPSAFBAGRTVLAMDPMWFTLRLIHFAIHQOLPKIIVERRMKMDVFFFF 879
 DB 877 LGVGCRLTPGLYHGRVLTCTDFWFTVRLAHIFVNNQOLPKIIVSKMKMDVFFFLFF 936
 QY 880 LSVMLVAVGVTTOALLPHDGLRWIFRRVLYRPLQIFGOIPLUDEIDEARV--NCSTH 936
 DB 937 LGVMLVAVGAVATEGLLRPRDSDPFIARRVFRPLQIFGOIPOEDMDVALMEHSNCSE 996
 QY 937 PLLLEDDSP-----SCPSLYANMLVTLVLTFTLVNVLNMLLAMSPTSQVQVGNATM 991
 DB 997 PGFMAHPFGAAGCTCVSQTANMLVLLVLLVILFVLVANILLVNLILAMESYTFGKQVNSDL 1056

QY 992 FWKFORYNLIVEYHERPALAPPFILLSHSLTLRRVFKK-----EAEHKREHLERD 1042
 DB 1057 YWKQGRYVLIIEPHSRPALAPPFITYSHLRLLRLQLCRRPSPQPSPALHEFRVYLSKE 1116
 QY 1043 LPDPLDQVNVVTWEYQKNFSLKMEKRRRDEGEVLRKTAHVRDFIAYLGLRQEKRI 1102
 DB 1117 ---AERLLTWESYHKNFLLARARDREEDSERLKTQSKVDLAKQLGHIREYFORL 1172
 QY 1103 KLESGQINYSVLVSVADVLAQG-----GGP 1129
 DB 1173 KYLEHEVQCSRVLGWVAEALSRSLALPPGP 1204

RESULT 13
 AAE20283
 ID AAE20283 standard; Protein, 1214 AA.
 XX AAE20283;
 AC 18-JUN-2002. (first entry)
 DT Human Trp9 protein.
 DE Human, prostate carcinoma associated protein; Trp9; Trp10a; Trp10b;
 KW transient receptor potential; calcium channel protein; Trp8a; Trp8b;
 KW molecular marker; endometrial cancer; uterine carcinoma; melanoma;
 KW gene; tumor; chorion carcinoma; lung cancer; antisense therapy.
 OS Homo sapiens.
 XX MO200210382-A2.
 PN 07-FEB-2002.
 PD 18-JUL-2001; 2001WO-EP08309.
 PF 28-JUL-2000; 2000US-221513P.
 PR (WISS/) WISENBACH U.
 PA (WISS/) WISENBACH U.
 XX P1 Wissenbach U;
 XX DR WPI; 2002-269013/31.
 XX DR N-PSDB; AAD32372.
 PT Novel isolated nucleic acid encoding human prostate carcinoma
 PT associated protein such as transient receptor potential 8a, 8b, 10a,
 PT 10b proteins, useful as molecular markers for diagnosing prostate
 PT cancer
 XX Claim 1; Fig 9A; 70pp; English.
 XX The invention relates to human prostate carcinoma associated proteins
 CC such as transient receptor potential (Trp) 8a, Trp8b, Trp9, Trp10a and
 CC Trp10b and nucleic acid molecules encoding such polypeptides. Trp8,
 CC Trp9, Trp10 are novel calcium channel proteins. Sequences of the
 CC invention are useful as molecular markers for diagnosing prostate
 CC cancer. Sequences of the invention, their antibodies, inhibitors and
 CC antisense molecules are useful for preventing, treating or ameliorating
 CC a prostate tumour, endometrial cancer (uterine carcinoma), tumour, a
 CC chorion carcinoma, cancer of the lung or melanoma. Polynucleotides of
 CC the invention are used in antisense therapy. The present sequence is
 CC human Trp9 protein.
 XX Sequence 1214 AA;
 SO

Query Match 39.8%; Score 2426.5; DB 23; Length 1214;
 Best Local Similarity 45.3%; Pred. No. 5.5e-221;
 Matches 531; Conservative 177; Mismatches 353; Indels 111; Gaps 26;

QY 26 GEVNFSGGKRRKGVFVPSGVAPSVLPDLLAEWHLPAPNLVSLVGEOPFAMKSWLR 85
 DB 76 GELDTGAGRKHSNFRSLSDRTDPAAVSLVTRTWGFRAPNLVSVLGGSGGPVLTQWLQ 135

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QY 86 DYLKRGVKAASSTGAMITLSATRGIAHNGOAVRDSHASTSTKRVAVAGMASLGRV 145
DB 136 DILRRGLVAAASSTGAMITVGTGLHTGIGHVAVARHOMASTG- GIKVAVAGVAPWGV 194
QY 146 LHRRLIEEAEQDFPVHY-----PEDDGSQGPLCSIDSNLSHFILVEPGRPGKGLTEL 200
DB 195 RNRDLINPKGSFPARYRKRGRDPD--GVQFP---LDVYSAFPLVDSTHCLGGENNF 249
QY 201 RLRLKHSIEQAGYGGTSGSIEIPVLCILVNDPNTLERISPAVEOAPWILVSGGIA 260
DB 250 RLRLSISYISQKTVGGTG-IDIPVLLLLIDDEKMLTRIENATQALPCLLVASGGGA 308
QY 261 DVLAAVLNPHILVP-----KVAEKQKPEKPSHMFEMEDIVMTKLONITSHOHL 313
DB 309 DCLAEITLED--TLAPSSGARGOEARIRREPK-----GDLEVLQAOVERIMRKELL 361
QY 314 TVYDEEOGSEELDTVILKALVACKSHSQEPQDYLDELKLAAMDVDAKSEIFNGDV 373
DB 362 TVYSSE-DGSEEFETIVLKALVKAC--GSSEASAYIDELRLAVAMNRVIDIASELFRDI 418
QY 374 EWKSCDLEEVNDALVSNKPEFVRLEVDNGADVADFLTYGRLOELYSVSRSKLLFDLIQ 433
DB 419 QMRSEFLIEASLMDALINDRPEFRLISHGLSLGFLTMRILAOLYSAPNSILIRNLID 478
QY 434 RKOEBRLTLAQL--CTQOAREPPAPRAFSLHVSRLVXDFLODAGRFGYODGRGRDR 491
DB 479 QASHSAGTAPALKGAALRPP-----DVGHVLRMLGKMKACAPRYSGGAMDPH 528
QY 492 RAEGPAPKPTGQKMLLDLNOKS-----ENPRDLFLVAVLONRHEMATYEWAMQO 542
DB 529 -----PGOGFESMYLSLDSKATSPSLDAGLGAPSDLLVALLNRAQMMYFEMGS 583
QY 543 EGVAAALAAKILIKENSHLETEAARATREA--KYERLALDFSCISYNSERAPALLY 600
DB 584 NAVSSALGACLLIRVARLEPDAAERKDLAFKEGEGVDIFGECYSSSEERARALL 643
QY 601 RNRCKSKTTCILHAEADAKAFEAHDGVOAFLTRIMWGDMAGRFILLGALFCFALV 660
DB 644 RRCPLMGATCLOAQADAPRAFAODGVOSLTLQKMGOMASTTIIYALVLAFFCPPLI 703
QY 661 YTNLTF--SEAPLRTGLEDLDDLDLDEKSPLYGLOSREVELAEPRAQD----- 712
DB 704 YTRLITFRKSEEPTEEBLE--FDMOSVINGESPVTADPAEKTPIGVRQSGRPCGG 761
QY 713 --RGRPAVFLTRKRFWGAIVTVFLGNVVMFAFLPLFTYVLLVDFRPPGSGPEVT 770
DB 762 RCGGRRC--LRMFHFGVPTIIFMGNVSYLLFLLFSRLVLDVFOFAP--PGLLEIL 816
QY 771 LTFWVTVLVEIRGOFPTDEDT-----HLVKKFTLVVGNMNMCDVVAIFLFI 819
DB 817 LTFWATLICEIRLOGLSGGGSLASGGPBGHASLSQRRLVLAOSMOCDDVALTCBU 876
QY 820 VGVTCMLPSAFAGRTVLAMDPMVFTLRIHIFAIHKOGLPKIIVERMKNDFEFLF 879
DB 877 LGVGCILTEGLYHIGRTVLCIDMVTVRLHIFTNKQGLPKIVSKMKOVFFLEF 936
QY 880 LSVMLVAVGVTGALLPHDGLRLEMTFRVLYRPYQIFQQLPLDEIDARV--NCSTH 936
DB 937 LGVWLVAVGAVATEGLRPRSDPSPILRRVFRPYQIFQIQDEMDVALMHSCSS 996
QY 937 PLLLESP-----SCPSLVANMVLIIIVTLLVNTVNLMLIIANFSYFOVQGNATM 991
DB 997 PGFWAHPGAQACTCVSYANMLVLLVLELVANLILNLIAMSFYFGVQGNASDL 1056
QY 992 FMKFORVNLIVEXHRRPALAPFILLSHSLTRRVFK-----EAHGRKHLERD 1042
DB 1057 YMAQGYRLIRFHSRPALEPTIVSHLRLLRQLCRRRSPQSPSPALEHRRVYLSL 1116
QY 1043 LPDPLDOKVVTWVOKENFLSKMEKRRDSEGEVLAKTARVDFIAKTYGILREDEKRI 1102
DB 1117 ----AERKLLTWESVHKENFLARADKRESDESRILKRTSQKDLAKQIGHIREYORL 1172

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QY 1103 KCLSEQINVCSTLVSSVADWLAQG-----GSP 1129
DB 1173 KVLREYVQCGSRVLGWAVALSRSLPDPGP 1204

RESULT 14
AAB85974
ID AAB85974 standard; Protein; 1129 AA.
XX
AC AAB85974;
XX
DT 30-NOV-2001 (first entry)
XX
DE Human TLCC polypeptide.
XX
KW TLCC; transient receptor potential; TRP; TRP-like calcium channel; human;
KW hepatotropic; cardiac; antiarteriosclerotic; antiinflammatory; vitruide;
KW cytosolic; analgesic; cerebroprotective; nootropic; neuroprotective;
KW gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1084..1129
FT /note= "the residues in this region are not indicated in
FT the sequence present in the sequence listing, but
FT indicated in the Figure"
XX
PN WO200162794-A2.
XX
PD 30-AUG-2001.
XX
PE 20-FEB-2001; 2001WO-US05529.
XX
PR 22-FEB-2000; 2000US-0510706.
PR 31-MAY-2000; 2000US-0583373.
PR 08-AUG-2000; 2000US-0634669.
XX
PA (MILL-) MILENNIUM PHARM INC.
XX
PI Glucksmann MA, Curtis RAJ, Lora JM;
XX
DR WPI; 2001-557700/62.
XX
DR N-PSDB; AAH76383, AAH76384.
XX
PT New isolated nucleic acid encoding a transient receptor potential-like
PT calcium channel for identifying modulators that can be used to treat
PT hepatic or cardiovascular disorders.
XX
PS Claim 14; Fig 1A-D; 160pp; English.
XX
XX
CC The invention provides isolated nucleic acids encoding a human transient
CC receptor potential (TRP) family member, called TRP-like calcium channel
CC (TLCC) polypeptide. The TLCC polypeptide can be expressed by standard
CC recombinant methodology. The TLCC polynucleotides and polypeptide are
CC used to identify modulators that can be used to treat a hepatic or a
CC cardiovascular disorder, such as liver fibrosis or atherosclerosis.
CC Other disorders that can be treated are hepatitis, liver tumors,
CC cirrhosis of the liver, hemochromatosis, liver parasite induced
CC disorders, central nervous system disorders, pain disorders, or
CC disorders of cellular growth, differentiation or migration. The TLCC
CC polynucleotides, polypeptide, protein homologs and antibodies to the
CC protein can be used in predictive medicine (e.g. diagnostic assays,
CC prognostic assays; monitoring clinical trials and pharmacogenetics).
CC Anti-TLCC antibodies can isolate TLCC proteins, regulate the
CC bioavailability of TLCC proteins, and modulate TLCC activity. The
CC present sequence represents the human TLCC polypeptide.
XX
SQ Sequence 1129 AA;
XX
Query Match 39.3%; Score 2394.5; DB 22; Length 1129;
Best Local Similarity 45.4%; Pred. No. 5..5e-218;
Matches 526; Conservative 174; Mismatches 348; Indels 11; Gaps 26;

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QY	39	KEVRPSSVAPSVLEPDLLEAENHLPAPNIVVLSVEEOPFAMKSVLBDVLKGLYKAOS	98
Db	4	QFLRLSDTDPRAVSVLWTRTWGFAFAPNIVVLSGGSGEPVLQTVLQDLIRGLVRAOS	63
QY	99	TGAMVILTSALRVGLARHVGQAVRDSHSLASTSTKRVAVVAGMASLGRVLRHRLLEBAQDF	158
Db	64	TGAMVITGGLTGTGRHVGAVARHDQMASTG-GTKVAMGVAPMGVVRBDTLINPKSF	122
QY	159	PVHV-----PEDDGSGOPLGSDENLSHFLIVEGPPGKGDGLTELRLLEKHSQRA	213
Db	123	PARRWCRDPED--GVQPP---LDVNYAPFLVDGTGCGGGENRFRRLSEYSIOQKT	177
QY	214	GYGCTGSIEIPLCLVNGDPTWTERISRAGEQAAPMVLIVGSGIAVLAAVLPQHL	273
Db	178	GVGGTG-IDIPVLLLLIDGDEKMLRINENATQAPCLLVVSGGAACIMTLEDD--TL	234
QY	274	VP-----KVAEKOPKEKPPSKHFSMEDIVRWTKLQNTSHQLLTVYDFEORGSEEL	326
Db	235	APGSGGARQGEHRDRIRRFPPK-----DGLLEVLAQAVRIMTRKELLTVYSGE--DGSEEF	288
QY	327	DTVILKALVAKCKSHSOEPODYDELKLAAMADRDYDIKSELPENDVEMKSCDLEEWVD	386
Db	289	ETIVUKALVAKC--GSSASAYLDELRLAIVANRVDIAOSELFRGDITQWRSHTLEASLMD	346
QY	387	ALVSNKEPEVRLFVYNGADVADFLTYYGLOELVRSVRSKSLFDLLQKOEABRLTLIAGL	446
Db	347	ALLNDRPEFVRLILSHGLSLGHFTLPMRLAQLYSAAPNSILRLNLDQASHAGTAKAPAL	406
QY	447	--GTOQAEPRAGRAPRPSLHEVSRVLKQFLDQACGFYQDERPGGRRAEKAPRAPPGQ	504
Db	407	KGGAALERP-----DGHVLRNLLGKMCAPRYPSGGAMPB-----PGGFGSES	451
QY	505	KMLLDLNGKS-----ENMPWDLFPMAYLONRHEMATFYMAWGOEGVAALAAACKIL	555
Db	452	MYLLSDKATSPSLDLAGQAPWSDLLMALLLNQAQAMFMFMEMGSNAVASLACALL	511
QY	556	KEMSHLETEABARATREA--KYERLALDLSEECYSNSEDARFALLVRRNCWSTTCLH	613
Db	512	RVMARLEBDABEBAARKDLAFEFEBMGVDLFECEYRSESEVRARLLLRCPMLMGATCLO	571
QY	614	LATEADAPAFPHDOVQAFTRIMQDMAAGPRLILGALFCFALVYTNLTTF--SEEA	671
Db	572	LAMQADAPAFRAQDOVSULTOKMGDMASTPPIALVALFPCPLITRLITTFKSSSE	631
QY	672	PLATGLEDLDLSDLETKSPLYGQSHVEBELVEAPRAQD-----RGRAVFLITR	723
Db	632	PTREBLE--FMDSDVINGEPGVGTADPAEKTPLVGVRQSGRGCCGGRCCGRCC--LRR	686
QY	724	WRKPMGAVVYPLGVNVMYFAFLPLFTYVVLVDFFRPQGSGBEVNTLYFVVFITVLEBI	783
Db	687	WFHFMGAVNTIFMGNVVSYLLFLLLSFRVLLVDFQPAR--PGSLLELLYFMAFTLLCABL	744
QY	784	ROGFEETDEDT-----HLVKKFPLVYGDNNKNCMDMVAIFLFIYVTCRMLPSAFB	832
Db	745	ROGLSGGGGSLASGSPRGHSLSSGRRLRYLADSNQCDVALTGFLLGVGCRGLPGLYH	804
QY	833	AGRTVYLANDFVNTRLTHIIRAHKQDCKPIIVERMKNKDVFELFPLSVMLVAVGVTTQ	892
Db	805	LGRVTLCIDFVWFTVRLHLHIFTVNKQDCKPIIVISKMKDKVFFELFELGVMLVAGVATE	864
QY	893	ALHPRHDLRLEMIFFRVRVLRPYLOFGQIPIDEIDEARV---NCSGTHLLEDSG----	944
Db	865	GLLRPRSDPFSILRRVFRPYLOFGQIPQEDMDVAMHENSNGSBEQFMWHPRGAQAG	924
QY	945	SCPSLYANVLYLLVTELLVTVNLVNLMLIAMFSYTFQVYVQGNATMFWKFORVNLIVEY	1004
Db	925	TCVQOYAMLVLLVLLVFLVANITLVNLLIAMFSYTFGVKQVGNSDLYMKQRYLIREF	984
QY	1005	HERPLARPEFLLSLSTLRRVFK-----EAHKEENLERDRLDQCVYVWE	1055
Db	985	HSRPLAPPELVISHRLRLKQLCRRPSPQDSSPALHFRYLLSK-----AERKLLTWE	1040

QY	1056	TVQENFFISKKKEKRRDSEGVLTAKTHARVDFINAKYGLAEQERIKCSQINVCVL	1113
DB	1041	SVHKEENFLMARDKRSEDSRLKRTSKVDLAKOLGKHIREYORLKVLEREVOQCSRV <td>1100</td>	1100
OY	1116	VSSVADVLAQG-----GGP 1129	
DB	1101	LGWVAEALSRGALLPGGP 1119	
RESULT 15			
ABG72088			
ID	ABG72088	standard; Protein; 1083 AA.	
XX	ABG72088;		
AC			
XX			
DT	11-FEB-2003	(first entry)	
XX			
DE	Human transient receptor potential (TRP)-like calcium channel (TLCC).		
XX			
KW	Human; transient receptor potential-like calcium channel; TRP;		
KW	TLCC; 18607; calcium signalling; growth; differentiation;		
KW	capacitactive calcium channel; store-operated calcium channel; SOC;		
KW	plasma membrane; calcium ion; cytosol; modulator; membrane excitability;		
KW	action potential; excitation; neurite outgrowth; synaptogenesis;		
KW	signal transduction; angiogenesis; cell proliferation; vascular tone;		
KW	gene therapy; diagnosis; cardiovascular disorder; atherosclerosis;		
KW	retenostis; endothelial cell disorder; tumor metastasis; porphiasis;		
KW	rheumatoid arthritis; diabetes; hepatic disorder; hepatitis; cirrhosis;		
KW	central nervous system disorder; Alzheimer's disease;		
KW	Parkinson's disease; multiple sclerosis; epilepsy; cancer;		
KW	cellular proliferation disorder; migration disorder; therapeutic.		
XX			
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	Region	1..1083	
FT	/note=	"This region is shown as SEQ ID NO:2 in the	
FT		sequence listing of the specification, but is only	
FT		a shorter version of SEQ ID NO:2 shown in figure	
FT		1"	
XX			
PN	US2002142377-A1.		
XX			
PD	03-OCT-2002.		
XX			
PF	20-FEB-2001; 2001US-0789481.		
XX			
PR	22-FEB-2000; 2000US-0510706.		
PR	31-MAY-2000; 2000US-0583373.		
PR	08-AUG-2000; 2000US-0634669.		
XX			
PA	(GLUCKS/) GLUCKSMANN M A.		
PA	(CURT/) CURTIS R A J.		
PA	(LORA/) LORA J M.		
XX			
PI	Gluckmann MA, Curtis RAJ, Lora JM;		
XX			
DR	WPI; 2003-102516/09.		
XX			
DR	N-PSDB; ABSS8041.		
XX			
PT	Isolated transient receptor potential-like calcium channel		
PT	peptide, useful for treating cardiovascular, hepatic, central		
PT	nervous system disorders, pain, cellular proliferation, or migration		
PT	disorder		
XX			
PS	Claim 14; Fig 1; 80pp; English.		
XX			
CC	The invention discloses an isolated transient receptor potential		
CC	(TRP)-like calcium channel (TLCC) polypeptide (18607). Calcium signalling		
CC	has been implicated in the regulation of a variety of cellular responses,		
CC	such as growth and differentiation. TLCC is a member of the capacitave		
CC	calcium channel group or store-operated calcium channel (SOC) which is		
CC	activated in the plasma membrane to import calcium ions from the		

extracellular environment to the cytosol. The nucleic acids, polypeptides and antibodies of TLCC are useful for detecting its presence in a sample, for identifying a compound which binds to it and identifying a compound which modulates its activity. Modulators of TLCC can be used to modulate membrane excitability, wave forms and frequencies of action potentials, thresholds of excitation, neurite outgrowth and synaptogenesis, signal transduction, angiogenesis, endothelial cell proliferation and vascular tone. The nucleic acid and polypeptide are also useful (using gene therapy) for diagnosing and treating cardiovascular disorders, such as atherosclerosis and restenosis, endothelial cell disorders, such as tumor metastasis, psoriasis, rheumatoid arthritis and diabetes, hepatic disorders such as hepatitis and cirrhosis, central nervous system disorders, such as Alzheimer's disease, Parkinson's disease, multiple sclerosis and epilepsy, cellular proliferation disorders, such as cancer, and growth, differentiation or migration disorders. TLCC can also be used in predictive medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomics) and in methods of treatment (e.g., therapeutic and prophylactic). The sequence presented is the human TLCC, 18607, protein.

Sequence 1083 AA;

Query Match 38.3%; Score 2335; DB 24; Length 1083;
Best Local Similarity 45.7%; Pred. No. 2.4e-212;

Matches 513; Conservative 165; Mismatches 338; Indels 106; Gaps 25;

```

QY 39 KVRVSSGAVPVLFFLLAEWHLPAKNI VSLVGESEFPAMKSWRLDRLRGVYAAQS 98
DB 4 QPLRLSDRTDPAVSVLVRITWGFRAPLVSVLGGSGGVPVLTWLTQDILLRGLVAAQS 63
QY 99 TGAMITLSALRVGLAHVGOAVRDHSLASTSTKRVVAVAGMASLGRVLRRIIEAEQDF 158
DB 64 TGAMITVGLHGTGIGHVAVRDHQMASTG-CTKVVAVAGVAPWGVRRRDTLTKPSGF 122
QY 159 PVHY-----PEDGSGQGPLCSLDSNLSHFILVEPGPPKGDGLTELRLLEKHISEQRA 213
DB 123 PARYWRGDPED--GVQFP--LDVYNSAFPLVDDGTHGCLGGENRFRLLRESYSIQOKT 177
QY 214 GVGCGTSIEIPVLCILVNDGPNLTERISRAVEQAAPWLLVNGSGIADVLAALVNOPIHL 273
DB 178 GVGCGT-IDIPVLLIDDEKMLTRLENATQAOLPCLLVAGSGAADCLAETLED--TL 234
QY 274 VP-----KVAEKQPEKPEPSKGFSEMDIVRWTKLLQNIITSHOHLITVYDFEQQSGEEL 326
DB 235 AGSGGARGGEARDRIIRREFPK-----GDLVQLAQVERIMTRKELLTYSSSE-DGSEEF 288
QY 327 DTVILKALVYAKKSHSQEPQDYLDELKLAVMADRVDAKSEIFNGDEVKSCDLEEVMD 386
DB 289 ETIVLKALVYAC--GSSEASAYLDELRLAVAMNRVDIAQSELFRGDIQWRSFHLIASLMD 346
QY 387 ALVSNKPEFVRFLFVNDGADVADFLTYGRLOELYRSVSRKSLPFDLLQKQEBARLTLAQL 446
DB 347 ALLNDPEFVRLLISHGLISGHFLTPWRLAQLVSAAPSNSLIRNLLDQASHSAGTYAPAL 406
QY 447 --GTQARPPAPPAFLSHEVSRVLKDFLODACRGFYODGRPGDRRAEKGPAPKPTQG 504
DB 407 KGAALRLRP-----DVGHVLRMLLGRKICAPRYPSGGAMDPH-----PGQFGES 451
QY 505 KMLLDLNQK-----ENPWRDLFLVAVLQNRHEMATYFWAMGOEGVAAALAAKTL 555
DB 452 MYLLSDKATSPSLDAGLPMSDLLWLLLNRAQMAMYFWMGSNNAVSAAGACLL 511
QY 556 KEMSHLETAEARARREA--KYERLALDLFSECYNSSEARAPALLVRRRCWSTKTLH 613
DB 512 RVVARLEPPAEARARKDLAFKEGQGVDFGECYRSSEVRAARLLLRCPIMGDATCLQ 571
QY 614 LATEADAKAFPAHDGVAQFLTRIMGDMAGTPIRLIGAFLCFALVYTNLITF--SEEA 671
DB 572 LAMQADARAFADQDQSLITQKMGDMASTPIWALVLAFCPPILYTRILTRKSEEB 631
QY 672 PLRTGLEDLDDSLDTEKSPLYGLQSRVELVEAPRAQD-----RGPRAVFLTR 723
DB 632 PTREBLE--FDMDSVINGEPVGTADPAEKTPGLGVPRQSGRPCGCGRCGRRC---LRR 686

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QY 724 WRKFWGAVTVLGNVWVYPAFLFETVLLVDERRPPQSGSEVTLTFVWFTLVLEBI 783
DB 687 MFHFWGAVTVTFMGNVSYLLFLLFSRVLLVDPRAP--FGSLELLLYFNAFTLLCEBL 744
QY 784 RQGFTEBDT-----HLVKKFTLYVGDNNKCDMAVLEFLIVGTCRMPLSAPE 832
DB 745 RQGLSGGGGSLASGGPGGHASLSQRLRLYLADSNNQCDLVALTCFLLGVGCRLLPGLYH 804
QY 833 AGRTLANDFWFTLRLHIFAIHKQIGPKIIVERRMKDVFPEFLFSLVWLVAAYGTTQ 892
DB 805 LGRVLCIDFWVFVRLHLFTVKNQIDLPKIVISKMKDVFPEFLFGLVWLVAAYGATE 864
QY 893 ALLHPDRLEWIFRRVLYRPIYLFQGIPLDEIDEARV---NCSTHPLLEDSP----- 944
DB 865 GILRRDDPESILRRVYRPIYLFQGIPOEDMVALMEHNSCSSEDFMAHPRGAQAG 924
QY 945 SCPSLYANWVILLVTLVTLVNLMLLIMPSYTFQVVOGNAWTFMFKFORVNLIVY 1004
DB 925 TCVSQYANWLVLLVTLVTLVNLMLLIMPSYTFQVVOGNAWTFMFKFORVNLIVY 984
QY 1005 HERPALAPFTLLSLTLTRVFK-----EAEKHKEHLERDLDPDLDOKVVTME 1055
DB 985 HSRPALAPFTVISHRLRLRLQLCRRPSPQSSPALSHFVYLSKE---AERKULTWE 1040
QY 1056 TVOKENPLSKMKRRRDSGEVLRKTAHVDPIAKYLGLE 1097
DB 1041 SVHKENFLAARARDRESDESLKRTSOKVDLAKQDLHIRE 1082

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Search completed: September 10, 2003, 09:39:43
Job time : 51 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: September 10, 2003, 09:38:44 ; Search time 21 Seconds
(without alignments)
2347.245 Million cell updates/sec

Title: US-09-834-792C-4

Perfect score: 6051
Sequence: 1 MODVQGRPRGPGDAEDRRE.....HRGGIDGWEQPGAGQPSDRT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	2041	33.5	1503	4	US-09-600-087-2
2	1562.5	25.7	1095	3	US-09-112-096-15
3	1228.5	20.2	1533	1	US-08-623-679-9
4	1228.5	20.2	1533	3	US-08-933-774-9
5	1228.5	20.2	1533	3	US-09-181-030-9
6	1228.5	20.2	1533	4	US-09-534-242-9
7	1228.5	20.2	1533	4	US-09-454-854-9
8	1228.5	20.2	1533	4	US-09-164-671-9
9	1150.5	18.9	1497	1	US-08-623-679-7
10	1150.5	18.9	1497	3	US-08-933-774-7
11	1150.5	18.9	1497	3	US-09-181-030-7
12	1150.5	18.9	1497	4	US-09-534-242-7
13	1150.5	18.9	1497	4	US-09-454-854-7
14	1150.5	18.9	1497	4	US-09-164-671-7
15	813	13.3	315	3	US-09-020-956-112
16	813	13.3	315	3	US-09-030-607-112
17	813	13.3	315	4	US-09-439-313-112
18	813	13.3	315	4	US-09-352-616A-112
19	813	13.3	315	4	US-09-232-148A-112
20	606	9.9	300	2	US-08-727-688-11
21	504.5	8.3	316	4	US-08-412-325-378
22	498	8.2	542	1	US-08-412-431-3
23	498	8.2	542	1	US-08-623-679-3
24	498	8.2	542	3	US-08-933-774-3
25	498	8.2	542	3	US-09-181-030-3
26	498	8.2	542	4	US-09-534-242-3
27	498	8.2	542	4	US-09-454-854-3

28	498	8.2	542	4	US-09-164-671-3	Sequence 3, Appli
29	333.5	5.5	201	4	US-09-461-325-175	Sequence 175, App
30	285	4.7	256	2	US-08-727-688-33	Sequence 33, Appl
31	221	3.6	742	4	US-09-500-123-12	Sequence 12, Appl
32	216	3.5	871	4	US-09-500-123-7	Sequence 7, Appli
33	210.5	3.5	1709	4	US-09-392-812A-6	Sequence 6, Appli
34	201.5	3.3	1619	4	US-09-392-812A-4	Sequence 4, Appli
35	186	3.1	1704	4	US-09-392-812A-2	Sequence 2, Appli
36	180	3.0	811	4	US-09-500-123-9	Sequence 9, Appli
37	171	2.8	116	4	US-09-461-325-375	Sequence 375, App
38	153	2.5	761	4	US-09-235-451-4	Sequence 4, Appli
39	150	2.5	968	3	US-08-651-999A-7	Sequence 7, Appli
40	150	2.5	968	3	US-09-385-752-7	Sequence 7, Appli
41	143.5	2.4	843	4	US-09-235-451-25	Sequence 25, Appli
42	142	2.3	839	4	US-09-667-422-4	Sequence 4, Appli
43	141	2.3	839	3	US-09-197-636-2	Sequence 2, Appli
44	141	2.3	839	3	US-09-197-636-8	Sequence 8, Appli
45	141	2.3	839	4	US-09-235-451-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1
US-09-600-087-2
; Sequence 2, Application US/09600087
; Patent No. 6548272
; GENERAL INFORMATION:
; APPLICANT: Shimizu, No. 6548272yoshi
; APPLICANT: Nagamine, Kenharo
; TITLE OF INVENTION: GENE CODING FOR A NOVEL TRANSMEMBRANE PROTEIN
; FILE REFERENCE: 11283-004001
; CURRENT APPLICATION NUMBER: US/09/600,087
; CURRENT FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: PCT/JP99/06289
; PRIOR FILING DATE: 1999-11-11
; PRIOR APPLICATION NUMBER: JP/321200/1998
; PRIOR FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: (320)...(344)
; NAME/KEY: TRANSMEM
; LOCATION: (750)...(773)
; NAME/KEY: TRANSMEM
; LOCATION: (794)...(818)
; NAME/KEY: TRANSMEM
; LOCATION: (867)...(891)
; NAME/KEY: TRANSMEM
; LOCATION: (900)...(924)
; NAME/KEY: TRANSMEM
; LOCATION: (932)...(956)
; NAME/KEY: TRANSMEM
; LOCATION: (1024)...(1048)
US-09-600-087-2

Query Match 33.5%; Score 2041; DB 4; Length 1503;
Best Local Similarity 36.8%; Pred. No. 2,1e-191;
Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;
QY 26 GEVNFSGGKRRKFRVPSGVAPSVLPDLLAEKHLPAPIVLVSLVGEQPFAMKSWLR 85
DB 128 GDIYFTGSLGQVKKVRSQDTPSSVYHLMTQMGDLPVPLLSVTGAKQVFMKPRK 187
QY 86 DVLKGLVKAQSGATWLTSLKRVGLARHGOAVRHSLSASTKRVAVAGMAGSLGRV 145
DB 188 SIFRGLVKAQSGATWLTSLKRVGLARHGOAVRHSLSASTKRVAVAGMAGSLGRV 247

146 LHRRIEAEQEDPVHYPEDDGSOGPLCSLDSNLSHFLVEPBGPKDGLTELRLE 205
 248 HREGLIHFTSGFPAEYIIDEBOG--QGNLCLCDSNHSFLVDGDGHGVGIVEPLRTRE 306
 206 KHISEORAGYGTGSIETPVLCLVNGDPNTERISRAVEQAAPMILVGGGADVLAA 265
 307 KEISEOTKERGGV-AIKIPICVVLGEGGTHTTIDNATNGTPCVAVGSGRADVLAQ 365
 266 LVNQP--HLVVKVAEKO--FKERPSGHFMEIDVVRPTKLLONTSHOHLTYVDPQ 320
 366 VMLPVSDDITSLIQKLSVFQEMET--FTESRIVENTTKI QDVRRRQLTVRBEK 423
 321 ESSEEDTVILKALVACKSHSQEPDYLD-ELKLAIVANDRYDAKSEIFNGDVEKSCD 379
 424 DGOQDVVAIQLALKASRSDHFGHEMNDHOLKLAIVANNRDIARSELFMEMQKRPD 483
 380 LEEVAVDALVSNKPEFVRLPVNDGADVADFLTYGRLOELYSVSRKSLFDLLQKQBEA 439
 484 LHPMTAALISNKPFEVLFLENGVQLKEFTWDTLLYENLDPSCLFHSKLOK----- 538
 440 RLTLAGLGTQOAREPAPG--PAFSLHEYSRLKDLQACGFGYODGRPGDRR----- 492
 539 -----VLVEDPERPACAPAPPLQMHVAQVRELSGFTQPLYPRHNDRLRLLPV 592
 493 -----AEKPAKRPFGQKWLIDLNQKSENPRDLFLVAVLQNRHEMATYFAMQ 542
 593 PHVKLVQGVSLRSLYKSSGHVTF-----TMDPIRDLIAVQNRRELGLIITWAGQ 646
 543 EGVAAALAAKILKENSHLETEAAR--ATREAKYERLALDLFSECYSNEBARAFALL 599
 647 DCIAALACSKILKEISEEDTDSSEEMALAE-EYEHRAIGVFTECYRKEEERAKKL 705
 600 VARNQMSKTTCGLHATEADAKAFPAHDGVOAFLRIMWGDMAAGPIRLILGAFICFL 659
 706 TVSEAMGKTTCQLALEAKMKFVSHGSIQAFILKVMGQSLVDNGLRVLCLMLAFPL 765
 660 VYTNLTTFSEBAPLRTGLEDLQDLSDLTEKSPLYGLQSRVSELVEAPRAQDGRPAVF 719
 766 LITGLISPREKR-----LQD-----VGTFA----- 786
 720 LITRMKMGADVTLFGLNVVMYFAFLFTYVLVLDVRRPPOGSGPSEVTLYFVVTIV 779
 787 ---RAAFPTAAVUVFHLNLSYFAFLCLFAVYLVMDFOV--PSCMCAIYLMFSLV 840
 780 LEEISGFEFTDDTHLYKFFLYVGNMKNKCDMVAFLFIVGTGCMLSAEBAGTVLA 839
 841 CEEKROLFYDPBECGLMKRAALYFSDFMKLDVGLILFVAGLTCRLIATLYPGKVLIS 900
 840 MDPVFTLRILHIFAIHKOLOGKIIIVEREMKDVFFFLFSLVWLVAVGVTTQALLPHD 899
 901 LDFILFCARLMIHFTISKTLGPRILIVKRMKDVFFFLFLAVVVSFCVAQALIHNE 960
 900 GLEWTFRRVLYRPIYQITGQTP--LDEIDEARVNS--THPLLEDSPSCS----- 948
 961 RAVDMLFRCVAVHSYTLIFGOIPGYIDGVNFPEHCSPNGTDPY----PRKPSDATQO 1016
 949 ---LYANWLYLILVFLVLTAVNLMLLITAMFSYTGQVQVGNATMWMKORNLIEYHE 1006
 1017 RAAPFWMVLTLCTLCTLFTNLILLNLITAMENYTFQVQVHEHDOQIMKORHDLLEHNG 1076
 1007 RPAAPFILLSHLSTLRRVFEKEAENKREHLEBDLPDLQKVVTVEVQKENFLSKM 1066
 1077 RAAPRPFILLSHLOFIRKRVILKTPAKHKOKNLEKNEBAILLSWILYKENVLOQR 1136
 1067 EKRRDSEBVLKTAHADVFLAKYV-----GGLREOKRIKLESQINYSVLVSS 1118
 1137 QCOQKORPEOKIEDISNKVDAMVDLIDLPKRSQSM---EQRSLAEQVAVQTAALAHM 1193
 1119 VADVLAQGGGRSSQHCQSGSOLVAD---HGGIDGWEPQ 1157
 1194 IVRTLASGFSSEADVPTLASQAAEBPDAEPGRKKTPEG 1235

RESULT 2
 US-09-112-096-15
 ; Sequence 15, Application US/09112096
 ; Patent No. 6194152
 ; GENERAL INFORMATION:
 ; APPLICANT: Reiner Laus
 ; APPLICANT: Michael H. Shapiro
 ; APPLICANT: Larisa Tsavaler
 ; TITLE OF INVENTION: Prostate Tumor Polynucleotide and
 ; TITLE OF INVENTION: Antigen Compositions
 ; FILE REFERENCE: 7636-0015.30
 ; CURRENT APPLICATION NUMBER: US/09/112,096
 ; EARLIER FILING DATE: 1998-07-09
 ; EARLIER APPLICATION NUMBER: 60/056,110
 ; EARLIER FILING DATE: 1997-08-20
 ; NUMBER OF SEQ ID NOS: 29
 ; SOFTWARE: faSeq for Windows Version 3.0
 ; SEQ ID NO 15
 ; LENGTH: 1095
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-112-096-15
 Query Match 25.7%; Score 1562.5; DB 3; Length 1095;
 Best Local Similarity 34.2%; Pred. No. 2.1e-144;
 Matches 378; Conservative 202; Mismatches 394; Indels 111; Gaps 27;
 26 GEVNFSGSKRGKRVPRVSGVAPSVLEFDLLAEWHLPAPMLVYSLVGEEDPFAMKMYLR 85
 95 GDIOGETYGGK-GKTIIRISCTDPAELIYELLQHWHLTPMLVLSVTGAKNFAKPRKR 153
 86 DVLRKGLVKAQOSTGAWILTSALRYGLAHVGOAVRDHSLASTSTKYVAVAGNASLGRV 145
 154 KIFSR-LVIYAKSKAMWIDGTHGLTKRYGEVVRDNTI--SRSEENI VAIIGIAMGV 211
 146 LHRRIE--EAQEDPVHYPEDDGSOGPLCSLDSNLSHFLVEPBGPKDGLTELR 202
 212 SNRDTLINCAEGFYLAQYLMDD-FTRDPLYIIDNNHTHLLVNGCHGHPTEAKLRN 270
 203 RLEKHISE--QAGYGTGSIETPVCLLVNGDPNTERISRAVEQAAPMILVGGSGI 259
 271 QLEKHISRTTIDSNVYG---KIPVFAOQGGKETIKAINTSIKNIPCVVGGSGRI 326
 260 ADVLAALVNOPIHLVPKVAEKQFKEKFS--KHFSMEDIVWTKLQNTSHOHLTYVD 317
 327 ADVASLVEVEDAPTSAAVKEKLVRFRTYSRLSEETSEMIKWLKEILDEGSHLTYIK 386
 318 FEQESSELDTVILKALVACKSHSQEPDYLDLKLAVANDRYDAKSEIFNGDVEKWS 377
 387 MEEADEIVSNALISYALYKASTSEQDKDNNGQLKLLBNQDLANDDEIFTNDRWES 446
 378 CDLEEVMDALVSNKPEFVRLPVNDGADVADFLTYGRLOELYSVSRKSLFDLLQ---R 434
 447 ADLQEVMTFALIKDPRKTVRLFLENGLWLRKFLTHDVLTFL-SNHSTVLVTRNLQIAKN 505
 435 KOEERLTLAGLGTQOAREPAPGPAFSLHEYSRLKDLQACGFGYODGRPG--DRRRA 493
 506 SYNDLILTF-----VMTLVANFR---RGFKKEBNGRDEMDI 539
 494 EKGPARKPTGQKWLIDLNQKSENPRDLFLVAVLQNRHEMATYFAMQOEGVAAALAAK 553
 540 E-----LHDVSPITRHPLOALFIWAILQNKKELSKVIEQTRGCTLAALGASK 587
 554 ILKEMSHLETEAARAREA--KYERLALDLFSECYNSEBARAFALLVRNRCKSTTC 611
 588 LKTLAKVKNIDINAEGSEBELANEYETRAVELFTECYSSDDEDLAQLLVYSCAAGGSGNC 647
 612 LHLATEADAKAFPAADVQVAFTRIMWGDMAAGPIRLILGAFALVYTNLTTFSEEA 671
 648 LELAVEATDQHTAPQVGNFLSKOMYGEISRTQNMWIIICLPIIPVGGGFSFRKK- 706
 672 PLRTGLEDLQDLSDLTEKSPLYGLQSRVSELVEAPRAQDGRPAVFLLTRMKFWGAP 731

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      MOLECULE TYPE:  protein
      us-08-623-679-9

      Query Match      20.2%; Score 1228.5; DB 1; Length 1533;
      Best Local Similarity 27.9%; Pred. No. 3.6e-111;
      Matches 356; Conservative 229; Mismatches 451; Indels 241; Gaps 38

      QY 40 FVRVPSGAPSVLFDLLLAEMHLPAFNLVLSVGEDEQPFAMKSWLRDYLRLKGLVKAQST 99
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
      Db 2 YIRSYDTKPPSLHLWMYKQMLEPKLLISVHGCLNFEHQPKLYQVFGKGLIDQAMTT 61
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

      QY 100 GAWILTSALRVGLARHVGQAVRDHSLASTSTKRVAVAVAGMASLGRVLRHRLLEBAQEDF 158
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
      Db 62 GAWLFTGGVSTGCVLSHGDALKDH---SSKRGRVCAIGALPAGV-----ENKEDLV 111
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

      QY 159 ---EVHYPEDDGSGQPLCSLDNSMLSHFELIVEPGRPGKDELTELRLERKHISEQ---- 211
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
      Db 112 GKDLTRYVQYIMSNLSKLSTVLSNNHTHTLLDNLGTLGGYGAEVKLRRLLEKHISIQKINT 171
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

      QY 212 RAGYVGSTGSLIEIPLYCLLVNGDPNTLERISRAVEQAQAWLLV---GSGGIADVLA----- 264
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
      Db 172 RLGGQ-----VPLVLGVVEGGFNVVSIIVEYLDQEBPPIPVVICDGSGRADILSFAKY 225
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

      QY 265 ---ALVNO---PHLLVPKVAEKQPKKEPKSKFMSWEDIVATKYLONITSHQHLTYVD 317
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
      Db 226 CEEGGINESLRQGLV---TIQTFNVYKAQSHQLFALIMCEMK-----KKELVTVFR 276
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

      QY 318 FEQSGSELDLVILKALVYKACKSHSQEPQDYLDLKLAAVANDRDVIAKSEIFNGDEVW-- 375
          ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

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Db      897 LYFVIMLVLMVMSFGVARGAIIHPBE-KPSWKLARNIFMYPMYIYGEVAFDQID----- 950
Qy      933 CSTDHLLLEDSPSC-----PSLVANMLVILLVTFILVTNVLNMLLIAMFS 979
Db      951 ----LYAMEINPPCGENLYDEEGKRLPPCIPGAMLTPLMACYLLVANILLVANLIAVFN 1006
Qy      980 YTFQVQGNATPMFMRFORNYLIVEYHERPALAPFILLSLTLRV---FKKEAEHRK 1036
Db      1007 NTFEEVKISNQVMKFORQOLMTFHDRVLPFPMIILSHIYIIMRLSGCRKCRKREDDQ 1066
Qy      1037 EHLEBDL-----PDLQKVVWTVQENFLSKMEKRRRDEGEVLAKTAHVPFIAXY 1091
Db      1067 EERDRGLKFLPDEDEIKLHFEEOCVQEHFREK-EDEQSSSDERIRVTSERVENMSMR 1125
Qy      1092 LGGLREOEK-----RIKLESQINYSVSVSSVADV-----LAQGGGPRSSQHC 1136
Db      1126 LEEINERETFMKTSIQTVDLRLAQLLELSNMVNVALENLAGIDRSDLIQARS-RASSSEC- 1183
Qy      1137 EGSQVLAADHRGIDGM 1153
Db      1184 EATYLLROSSINSADGY 1200

RESULT 4
US-08-933-774-9
; Sequence 9, Application US/08933774A
; Patent No. 6025137
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
; FILE REFERENCE: 07314/004003
; CURRENT APPLICATION NUMBER: US/08/933,774A
; EARLIER FILING DATE: 1997-09-19
; EARLIER APPLICATION NUMBER: US 08/623,679
; EARLIER FILING DATE: 1996-03-29
; EARLIER APPLICATION NUMBER: US 08/412,431
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1533
; TYPE: PRF
; ORGANISM: Homo sapiens
US-08-933-774-9

Query Match      20.2%; Score 1228.5; DB 3; Length 1533;
Best Local Similarity 27.9%; Pred. No. 3,6e-111;
Matches 356; Conservative 229; Mismatches 451; Indels 241; Gaps 38;

Qy      40 FVRVPSGVAHSVLFULLLAEMHLPANLVSLVGEQPPAMKSWLRDVLRKGLVYRAQST 99
Db      2 YRVSVDTRKPDLSLHLMVMDQWOLEPKLLISVHGQIQNFEMQPKQVFGKGLIKRAMTT 61
Qy      100 GAMILTSLRVGLARHVGAVRDSHSLASTKRVAVAVGMASIGRVLHRIIEAOEDF- 158
Db      62 GAMITFGVSTGVISVIGALKDH---SSKSRGRVATIGIAPMGV-----ENKEDLV 111
Qy      159 ---PVHYPPEDGSGQGPLCSDLSNLSHFLVBERPBGKDGJLELRLEKHISEO--- 211
Db      112 GKDVTRVYQTMENPLSKLSVLNNSHTHFILADNGTIGKYGAEVKLRRLLEKHIISOIKINT 171
Qy      212 RAGVGTGSIETIPVLCILVNGDPNTERISRAVEQAAPWLILV---GSGGIADVLA----- 264
Db      172 RLGGG-----VPLVGLVVEGGPNVSVILEYLQEEPPPIPVVICDSSGASDILSPAHKY 225
Qy      265 ----ALVNO---PHLLVPKVAEKQFKEKPPSKHFSMEDIVRWTKLLQNTSHOHLTVYD 317
Db      226 CEEGGIINSLAEQOLV--TIQKTFYNNQAQSHOLFALIMECK-----KKELVTVYR 276
Qy      318 FEOEGSEELDTVILKALVACKSHSQEPQDYLDELKLAVAMRVDIKSEIFNGDEVW-- 375
Db      277 MSEGGQODIEMALITALLKG--TNVSAF-----DQSLSLAMNRVIDIARSOIFVFGPHWTP 330

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Qy      376 -----KSCD----- 379
Db      331 LGSILAPRDSKATEKEKPRPATTKGGRKGGKGGKGVKKEVEEBEEDPRKIELMNVNA 390
Qy      380 LEEVVDALVSNKEFEVRLPVQNGADVADFLTYYGLOELYSVSRKSLFDLLQKQEDA 439
Db      391 LEQAMLDALVLDVDRVFKLLIENGVMQHFLLTPILEELVYNTLRGPPTLHLVYADVKS 450
Qy      440 RLTLAGLGTQARERPAERPAF--SIHVSVNLDFLODAR-----GFYQD 484
Db      451 NL-----PDYHISLIDIGLVLEYLMGGAAYRCNTRKQFPTLYNNLHGP 494
Qy      485 GRP-----GDRRAEKGPAKPTGQKMLLDN-----QKSENPWRDLFLMAVLQNR 530
Db      495 KRPKALKILGMEDDEPPAKGKKKKKKKEEEDIDVDVPAVSRFQYPPHELMVMAVLKMR 554
Qy      531 HEMATYFWAMQOEGVAALAAKILIKENSHLETEEA-----RATEAKYERLALDLF 584
Db      555 QKMAVFLMQGEESMAKALVACKLYKAMAHESSESDLVDDISQDLNNSKDFGQLATELL 614
Qy      585 SECYNSARAFALLVRRNRCMSKTCGLHATEADAKAFPAHDGQAFLTRIMWG--DMA 642
Db      615 DQSYGHDEQIAMKLTLYELKNWMSNTCKLVAAGHRDFIAHTCSQMLTDMWGRLRMR 674
Qy      643 AGTPIRLGAFPLCFALVYTNLITFSEBAPRTGLEDDQDLSLDTESPLYQLSRYEE 702
Db      675 KNPGKLVIMGILLPFTILFLEFRY-----DDPSYOTSKEDEGKXEKEEN 720
Qy      703 L--VEAPRAQD-----RGPRAVFLTRMRKFWCAPTVLGVNVVYAFLEFTYLL 754
Db      721 TDANADASRRKDEBENEKKORSIPGKICEFYNAPIVKFWFYISYGLYLLFFNVYIL 780
Qy      755 VDFRPPGSGEPETLVFWVFTVLEIRGFFDEBETHLYKKRTLVVGNMNCMDVA 814
Db      781 VRM--DCWPSLQETIVSYVSLALEKIRE-ILMSEBCKLSQIKVWLQETMINITDVA 836
Qy      815 IFLFIVGTGCMILBSAFBA-GRTVLAMDPMVFTLRLLHIFAIHKQIGPKIIVERMMDV 873
Db      837 ISTPMIGAILBLQNPYMGKGRVICYVDIIFWYIRVLDIFGVNKYLGIVMMIGQMIDM 896
Qy      874 FFFLEFLSVMLVAVGVTTQALLPHDGRLEW-IFRRVLYRPLYQIFGOIPLDEIDEARVN 932
Db      897 LYFVIMLVLMVMSFGVARGAIIHPBE-KPSWKLARNIFMYPMYIYGEVAFDQID----- 950
Qy      933 CSTDHLLLEDSPSC-----PSLVANMLVILLVTFILVTNVLNMLLIAMFS 979
Db      951 ----LYAMEINPPCGENLYDEEGKRLPPCIPGAMLTPLMACYLLVANILLVANLIAVFN 1006
Qy      980 YTFQVQGNATPMFMRFORNYLIVEYHERPALAPFILLSLTLRV---FKKEAEHRK 1036
Db      1007 NTFEEVKISNQVMKFORQOLMTFHDRVLPFPMIILSHIYIIMRLSGCRKCRKREDDQ 1066
Qy      1037 EHLEBDL-----PDLQKVVWTVQENFLSKMEKRRRDEGEVLAKTAHVPFIAXY 1091
Db      1067 EERDRGLKFLPDEDEIKLHFEEOCVQEHFREK-EDEQSSSDERIRVTSERVENMSMR 1125
Qy      1092 LGGLREOEK-----RIKLESQINYSVSVSSVADV-----LAQGGGPRSSQHC 1136
Db      1126 LEEINERETFMKTSIQTVDLRLAQLLELSNMVNVALENLAGIDRSDLIQARS-RASSSEC- 1183
Qy      1137 EGSQVLAADHRGIDGM 1153
Db      1184 EATYLLROSSINSADGY 1200

RESULT 5
US-09-181-030-9
; Sequence 9, Application US/09181030
; Patent No. 6251597
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION

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1  TITLE OF INVENTION: AND TREATMENT OF TUMOR PROGRESSION
2
3  FILE REFERENCE: 07334/004005
4
5  CURRENT APPLICATION NUMBER: US/09/181,030
6
7  CURRENT FILING DATE: 1998-10-27
8
9  EARLIER APPLICATION NUMBER: US 08/862,442
10
11  EARLIER FILING DATE: 1997-05-23
12
13  EARLIER APPLICATION NUMBER: US 08/623,679
14
15  EARLIER FILING DATE: 1996-03-29
16
17  NUMBER OF SEQ ID NOS: 10
18
19  SOFTWARE: FastSeq for Windows Version 3.0
20
21  SEQ ID NO 9
22
23  LENGTH: 1533
24
25  TYPE: PRT
26
27  ORGANISM: Homo sapiens
28
29  US-09-181-030-9

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Query Match	20.2%;	Score 1228.5;	DB 3;	Length 1533;
Best Local Similarity	27.9%;	Pred. No. 3.6e-11;		
Matches 356;	Conservative 229;	Mismatches 451;	Indels 241;	Gaps 38

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QY 40 FVRPSPGVAVSFLFEDLLMEHLPAENVSLVSGEOPRPMKSMYLDRLRGGLKAAQST 93
Db 2 YIRSVYDTKEDSLIHLMAVCKOMLEPKLLISVHGLQNEQPKKQYFGGLIKAAMTT 61
QY 100 GAWILTSALVGLARHVGQAVRDHSLASTSTKYRVAVGMAISGLVTHRRILTEAOEDF- 156B
Db 62 GAWILTCGVSTGYISHVGDALKDH---SSKSGRCALIGIAPMGV-----ENKEDLV 111
QY 159 ---PVHYBEDDGGSGGRLCSDBNSHLFLVEBPGRKDGDTLETRLRLKHSIQ--- 211
Db 112 GKDVTRYQWMSNPRLKSLVANSNHHFLIADNGTLGKGAHEVKRLRLLEHISLOQINT 171
QY 212 PACTGGTSGLEIFVCLLVNGDPNTLERISRAVEDAAPMLIV--GSGGIADVTA---- 264
Db 172 RLGGG-----VPLGVIVGEGPNVSVILEYLEOEPPPIVPCDGSGRADILSPAHKY 225B
QY 265 ----ALVNO--PHLLVPKAEKQPEKPSHGFSMEDYKRTKLQNTSHQHLTYVD 317
Db 226 CEEGGIINESLRBQLV--TIQTFVYNAQSHQFALIMECK-----KKELVTVFR 276B
QY 318 FEOGSEELTVLKLKLVACKSHSGEOPDYLDELKLAVAMRVDAKSELFNQDVM-- 375B
Db 277 MGSBGQODIEMALLTALLG--TNVSAP---DQSLTAMNRVDIARSOIFVEGPHPTP 330
QY 376 -----KSCDD----- 379B
Db 331 LGSIAAPTDSKATEKEKPPMATTKGSGKGGKGGKKYKKEVEEETDPKRIELLMVNA 390B
QY 380 LEEVMDALVSNKPEFVRLFVNDGADVADFLTGYRLOEILYRSVSRKSLFLLORKOEA 439B
Db 391 LEOQMDALVLDREVDFVKLLIENGVMQHFLITPRLEELVNTRLQRPNTLHLVRDYKS 450B
QY 440 RLTLAGLGTQOAREPPAPPAF--SIHEVSRLKDFLODACR-----GFYOD 484B
Db 451 NL-----PDYHISLIDIGLVEYLMGAVRCNVTNRGNFTLVNLFGR 494B
QY 485 GRP-----GPRRAEKGPAKRPFGQXMLDLN-----OKSENPRDILFLAVYQNR 530B
Db 495 KRPRALKLIGMEDEBPAPGKKKKKKKEEEDIDVDPAVSRFQYPRHELMVAVLMKR 554B
QY 531 HENATFYMAWGQGVAAALAAACKIKEMSHETDEAA-----RATEAKYEBELADLF 584B
Db 555 QKNAVFLMORGESNMKALVACKLYKAMAHSSBSDLVDISODLDNNSKDFGLALELL 614
QY 585 SECYSNSEARAFALVRRNRCSKTTCLILATEADAKAFPAHDGVOAFLTRIMWG--DMA 642B
Db 615 DQGYKXDEQJAKMLLYVELKMSNSSTCLKLAAGHGRFIAHTCSQMLITMMGRIMR 674B
QY 643 AGPIILRLIGALCFALVYTNLITSEEARPLRTGLELDQDDSDLTEKSPLYQSHVEE 702B
Db 675 KNFGLKVIWMLILPILFLFEPRTY-----DDFSYQTSIENEDGKEKEEN 720B
QY 703 L---VEAPRQGD-----GRPAVFLITTRMKFGQAPVTVLGVNVMTAFLEFLTYVLL 754

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Db      721 TDANMADASRKDEENEHKKORSIIGTRKCEFNAPYKPFMYTISYIGLLEFFNYVL 760
Qy      755 VDFRPPGPGSGPEVTLTFWVFTLVLEIRGCFTEDEDTHLVKKFTLVYGDNNKCDMA 814
Db      781 VRM---DGMPSIQOEWIVISYIATSLALEKIRE-ILMSEPGKLSQKI KVMLOEYWNITDLVA 836
Qy      815 IFLFIYGTCCMLPAPFAFA-GRTVLAMDENVFTLLNHFALHKOLGPKIYVERMKUY 873
Db      837 ISTEFGIGILRIONOPYMGCGRVICVDIIIFYIVLDFEGNKKYLGVPVMMIGKKMIDM 896
Qy      874 FFFLFFLSVMIWAVYVTTQALHLPBDRLEW-IFFRVLYRPYIQIFGOIPLDEARVN 932
Db      897 LYFVIMLVLMSPVARQALIHPEE-KPSWLTANRIFMPYMWIYGEVFAOID----- 950
Qy      933 CSTHPLLEDSPPSC-----PSLVANMLVILLVTFLLVTVNLVNLMIAMS 979
Db      951 ----LYAMEINPCCGENTLYDEBGRKLPICIPGAMTLPALMACYLLVANILVNLIAFVN 1000
Qy      960 YTFQVVOGNAMTFWFCORYNLIVENHERPALARPITLISHLSLTLRV--FKKEENKR 1033
Db      1007 NTFPEVKSISNOQWFCORYOLIMTHDRVLPMPMIIISHYIITMRLSGRCKRKEGQO 1066
Qy      1037 EHLERDL-----PDLDQKVVTWETVQKENFLSKKEKRRDSEGEVLRKTAHVDFIAXY 1099
Db      1067 EERDRGLKFLTSDDELKRLHERBECOVGBHPEK-EDEOQSSDERIRNTSERVEWMSMR 112
Qy      1092 LGLGREOK-----RIKLESQIINCSVLVSVADY----LAQGGGRSSOHCG 1133
Db      1126 LEEINERETFMKTSLOTVDLRLAQLEELSNRMVNALENLAGIDRSLQARS-RASSEC- 1188
Qy      1137 EGSQVLVADHRCGIDGW 1153
Db      1184 EATYLRQSSINSADGY 1200

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RESULT 6
US-09-534-242-9
; Sequence 9, Application US/09534242

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GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
TITLE OF INVENTION: AND TREATMENT OF TUMOR PROGRESSION
FILE REFERENCE: 07334/004004
CURRENT APPLICATION NUMBER: US/09/534,242
CURRENT FILING DATE: 2000-03-23
EARLIER APPLICATION NUMBER: US 09/164,671
EARLIER FILING DATE: 1998-10-01
EARLIER APPLICATION NUMBER: US 08/862,442
EARLIER FILING DATE: 1997-05-23
EARLIER APPLICATION NUMBER: US 08/622,679
EARLIER FILING DATE: 1996-03-29
NUMBER OF SEQ. ID NOS.: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 1533
TYPE: PRT
ORGANISM: Homo sapiens
US-09-534-242-9

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Query Match          20.2% Score 1228.5 DB 4 Length 1533;
Best Local Similarity 27.9%; Pred. No. 3.6e-11;
Matches 356; Conservative 229; Mismatches 451; Indels 241; Gaps 38;

QY      40 FVRVPSGVAPSVLEPDLTLAEWHLPAPLVVSYLVEEQEPFAWKSMRLDVLRLKGLVKAAQST 99
       ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      2 YIRSYDTTKPDSLHLMLVKKMQELEPKLLLSVHGGLGNFENQPKYLKVFGGGLLKAAWTT 61

QY     100 GAMILTSALRVGLARHGOAVRDHSLASTSKTVRVVMGMASLCGRVLMRRILIEAOEFD- 158
       |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      62 GAMIFGTGVSTGVSHVGDAIKDH---SSRSRGRCVALGIAPMIV-----ENKEDVL 111
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Db      495 KRPRALKLIGMEDDEPRPAKGGKKKKKEEIDIDVDBAVSRFOYPPHELMVMAVLKMR 554
Qy      531 HEMATYFPMAGQEGVAALAAACKILKEMSHLETEAEA-----RATEAKYERLALDLF 584
Db      555 QKMAVFLMQGSEEMAKKLVAACKLYKAMAHSESSEDVVDIDISODLDNNSKDGQALBEL 614
Qy      565 SECYSNSEARAFALLVRNRCMSKTTCHLATEADAKAFPAHDGVOAFLTRIMWG--DMA 642
Db      615 DOSYGHDEQIMAKLLTYELKXMSNSTCLKLAVAAGHGFIAHTCSQMLTDMWRMLNR 674
Qy      643 AGTPILRLGAFLCFALVYTNLITFSEBAPLRTGLEDLDODLSLDEKSPLYGLQSRVE 702
Db      675 KNPGLKVMIGILLPPTILFLEFRTY-----DPSYQTSKENDGKKEEEN 720
Qy      703 L---VEAPRAQD-----RGPRAVELLTRMRKMGAPVYFLGAVVMYFAFLFTYVL 754
Db      721 TDANADASRKGDENEHKKORSIPICTKICEFNAPYKFWFYIISYGLYLLFNYYIL 780
Qy      755 VDFRPPGPGSPREVTLTFWFTLVLEIRGQFTDEDTHLVKFETLYVGDNMKNCDMVA 814
Db      781 VRM---DGMPSLQEWIVISYISLAEKIRE--ILMSEPGKLSQKIKVMLOEYWNITDLVA 836
Qy      815 IFLFIVGTQMLPSAFEA--GRTVLAMPVFTLLIHFAHKOGLGPKIIVERMMDV 873
Db      837 ISTEMIGALIRLQNOPMGYGRVICYVDIIFWYIRVLDIFGVNKYLGPRYMMIGMMIDM 896
Qy      874 FFFLFLSVMLVAVGTTQALLPHDGRLEW--IFRVLVRYPYLOIFGOIPLDEIDARVN 932
Db      897 LYFVIMLVLMSPGVARQALHPEE--KPSWKLARNIFMPYMWYGEVADQID----- 950
Qy      933 CSTHLLIEDSPSC-----BELYANMLVILLVTLVTVLLMNLIIAMS 979
Db      951 ----LYAMEINPPCCENLYDEEGKRLPCIPGAMLTPLAMCYLLVANILLNIIAVFN 1006
Qy      960 YTFQVVOGNATPMKFORNYLIVERHPALAPRILSHSLSTARV---FKKAENKR 1036
Db      1007 NTFEEVKISNOVMFQRQLMTFDRPVPRLPMLISHYIIIMRLSGRCRKKREDQ 1066
Qy      1037 EHLERDL-----PDPLDQKVMTVETOKENFLSKMEKRRDSEGEVLRKTAHRVDFIAKY 1091
Db      1067 EBRDGLTLFLSDEBLKHLHEFEBCVQEHFREK--EDEQSSDSBRIRKITSERVNMSMR 1125
Qy      1092 LGLREQEK-----RIKLESQIYNCSVLVSVADV---LAQGGGPRSSOHG 1136
Db      1126 LEEINERETFMKTSIQTVDLRLAQLEELSRMVALLENLAGIDRSDLLQARS--RASSEC- 1183
Qy      1137 EGSQVLADHRGIDGM 1153
Db      1184 EATYLLRQSSINSADGY 1200

RESULT 8
US-09-164-671-9
; Sequence 9, Application US/09164671A
; Patent No. 6372896
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
; FILE REFERENCE: 0734/004004
; CURRENT APPLICATION NUMBER: US/09/164,671A
; CURRENT FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: US 08/862,442
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: US 08/623,679
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 1533
; TYPE: prt
; ORGANISM: Homo sapiens
US-09-164-671-9

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Query Match      20.2%; Score 1228.5; DB 4; Length 1533;
Best Local Similarity 27.9%; Pred. No. 3,6e-111;
Matches 356; Conservative 229; Mismatches 451; Indels 241; Gaps 38;

Qy      40 FVRVPSGAVSVLPFDLLIAEWHLPAPNLVSLVEGEOPFPAKSWLRDLRGVLKVAOST 99
Db      2 YIRVSYDTPKPDSSLHLMKWDQLELPKLLISVHGGLQNFEMQPKLYQVFGGLIKAMATT 61
Qy      100 GAWILTSALRGVLAHVQAVRDSHLSASTKVVAVVNGMSLGRVILHRRLLEEQGEPE- 158
Db      62 GAWLFTGSGVSTGVSHWDALKDH---SSKSRGRCALGIAPWGVV-----EKEDLV 111
Qy      159 ---PVHYEDDDGGGQGPLCSIDNSLHFIYVPEPPGKGDLTJELRLKHSIQ----- 211
Db      112 GKDVTRYVQVMSNPUSKLSVLANSHHTIADNGLTKGYAEVLRLELGHISIQKINT 171
Qy      212 RAGYGTGSGIEIPVLCILYNGDPNTLERISHAVEQAAPWLLV--GSGGIADVLA----- 264
Db      172 RLQGG-----VPLVGLVVEGPPNVSVILEYLOEPPPIPVICDGSGRASDILSFAHY 225
Qy      265 ----ALVNG---PHLYPKVAEKQEKFPKSHSWEDIYVWTKLONITSHOHLTYVD 317
Db      226 CEEGILNESLREQLLV--TIQTFNNKQAOSHQFALIMCCK-----KKELVTVFR 276
Qy      318 FEOGSEELDVILKALVKAACKSHQEPQDYLDLKLAVADRYDIAKSEIFNGDVEW-- 375
Db      277 MGSEGOQDIEAAILTALLKG--TVNSAP---DQSLALANRRVDIARSOIFVGGPHWTP 330
Qy      376 -----KSCD----- 379
Db      331 LGSILAPPTDSKATEKEKPPMATTKGGRGKGGKGVKEVEEBETPRKIELLMVNA 390
Qy      380 LEEVNVVALYNNKEFPRLFYDNGADVADFLTTRGLQELYSVSRKSLLPOLLQKQSEA 439
Db      391 LEQAMLDALVDRDVFVCLLENGVMQHFLTIRLEELVYTRLRGPPNTLHLVDRVKS 450
Qy      440 RLTLAAGTQOARPPAPPAF--SLHEVSVLDFLODACR-----GFFQD 484
Db      451 NL-----PRDHYSLIDIGLVEYLMGAYRCYTRKNFTLYNNLFGP 494
Qy      485 GRP-----GDRRAEKGPAPKPTGQKMLLDN-----QKSENPWRDLFLMAVLQNR 530
Db      495 KRPRALKLIGMEDDEPRPAKGGKKKKKEEIDIDVDBAVSRFOYPPHELMVMAVLKMR 554
Qy      531 HEMATYFPMAGQEGVAALAAACKILKEMSHLETEAEA-----RATEAKYERLALDLF 584
Db      555 QKMAVFLMQGSEEMAKKLVAACKLYKAMAHSESSEDVVDIDISODLDNNSKDGQALBEL 614
Qy      585 SECYSNSEARAFALLVRNRCMSKTTCHLATEADAKAFPAHDGVOAFLTRIMWG--DMA 642
Db      615 DOSYGHDEQIMAKLLTYELKXMSNSTCLKLAVAAGHGFIAHTCSQMLTDMWRMLNR 674
Qy      643 AGTPILRLGAFLCFALVYTNLITFSEBAPLRTGLEDLDODLSLDEKSPLYGLQSRVE 702
Db      675 KNPGLKVMIGILLPPTILFLEFRTY-----DPSYQTSKENDGKKEEEN 720
Qy      703 L---VEAPRAQD-----RGPRAVELLTRMRKMGAPVYFLGAVVMYFAFLFTYVL 754
Db      721 TDANADASRKGDENEHKKORSIPICTKICEFNAPYKFWFYIISYGLYLLFNYYIL 780
Qy      755 VDFRPPGPGSPREVTLTFWFTLVLEIRGQFTDEDTHLVKFETLYVGDNMKNCDMVA 814
Db      781 VRM---DGMPSLQEWIVISYISLAEKIRE--ILMSEPGKLSQKIKVMLOEYWNITDLVA 836
Qy      815 IFLFIVGTQMLPSAFEA--GRTVLAMPVFTLLIHFAHKOGLGPKIIVERMMDV 873
Db      837 ISTEMIGALIRLQNOPMGYGRVICYVDIIFWYIRVLDIFGVNKYLGPRYMMIGMMIDM 896
Qy      874 FFFLFLSVMLVAVGTTQALLPHDGRLEW--IFRVLVRYPYLOIFGOIPLDEIDARVN 932
Db      897 LYFVIMLVLMSPGVARQALHPEE--KPSWKLARNIFMPYMWYGEVADQID----- 950

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Db 1032 ERDGLKFLPSDEELKRLHEEEOCVQEHFREK-EDEQSSSDEIRITSRVENMRL 1090
 Qy 1093 GGLREOEK-----RIKLESQINYSVLVSSVADY-----LAQGGPRSSOHGE 1137
 Db 1091 EBNERTFPMKTSLOTVDRLAQLLEELSNRMVNALENLAGIDRSLIQARS-RASSEC-E 1148
 Qy 1138 GSQLVADHRGGIDGW 1153
 Db 1149 ATYLLROSSINSADGY 1164

RESULT 10

US-08-933-774-7
 ; Sequence 7, Application US/08933774A
 ; Patent No. 6025137
 ; GENERAL INFORMATION:
 ; APPLICANT: Shyjan, Andrew W.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
 ; FILE REFERENCE: 07334/004003
 ; CURRENT APPLICATION NUMBER: US/08/933,774A
 ; EARLIER FILING DATE: 1997-09-19
 ; EARLIER FILING DATE: 1996-03-29
 ; EARLIER APPLICATION NUMBER: US 08/623,679
 ; EARLIER FILING DATE: 1996-03-29
 ; EARLIER APPLICATION NUMBER: US 08/412,431
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 7
 ; LENGTH: 1497
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-08-933-774-7

Query Match 18.9%; Score 1150.5; DB 3; Length 1497;
 Best Local Similarity 27.4%; Pred. No. 1.8e-103;
 Matches 349; Conservative 216; Mismatches 436; Indels 275; Gaps 39;

Qy 40 FVRVPSGVAPEVLPDILLAEWHLPAPNLVSLVGEEOEPFAMKSMRLDVLKGLVKAQST 99
 Db 2 YIRSYDTKPSLHLWKMDQWLEPKLLSVHGLQNFEMQPKKQVFGKGLTKAAVTT 61
 Qy 100 GAWILTSALRGLARHVAQVARDHSLASTSTKRVVAVGMAASLGRVLRRLIEAOEDF 158
 Db 62 GAWIFGTGVSIGVISHVGDALKH---SSKSRGRVCAIGIAPKGIV-----ENKELV 111
 Qy 159 ---PVHYPEDDGGQGPLCSIDSNLSHFILVPEPGKGDGLTELRLLEHISEQ--- 211
 Db 112 GKDVTRYVQTMNSPLSKLSVLNNSHTFILLDNGTLGKYGAEVLRRLLEHISLQKINT 171
 Qy 212 RAGYGTGSIETIPVLCILVNGDPNLTLEISRAVQAAPMLLV---GSGGIADVLA----- 264
 Db 172 RLGGG-----VPLVGLVNBGPVNSIVLELQEBPIPVICDGGSRASDILSPAHKY 225
 Qy 265 ---ALVNO---PHLVKVAEKOPEKEKPSKHSWEDIIVWTKLQNTSHOHLTVYD 317
 Db 226 CEEGGIINSEIREGLLV--TIQKTFNNKAKSHOLFALIMCKM-----KELVYVER 276
 Qy 318 PEQGGSELDVTIILKALVKACKSHSQEPODYLDDELKLVANDRVDAKSEIFNGDVEN-- 375
 Db 277 MGSEGOODIEMAILTALIKG--TVNSAP---DQSLALANRVDIARSOIFVGPHTP 330
 Qy 376 -----KSCD----- 379
 Db 331 LGSILAPPTDSVATKEKKPPMAATTKGGKGGKGGKGGKVEEVEETDPRIKILLNWNVA 390
 Qy 380 LEEVNVADLVSNKEFEVRLFYDNGADVADFLTYGRLOELYSVGRKSLIFDLQKOEBA 439
 Db 391 LEQMLALVADRVDFYKLLIENGVMNHFLITIRLEELVYTRIGPNTLHLVARDVKS 450
 Qy 440 RLTLAGLGTQOARREPAPGPAF--SLHEVSVLVKDFLODACR-----GFYOD 484

Db 451 NL-----PPDYHISLIDIGLVEYLMGAGVRCVYTRKNNFTLYNNLFGP 494
 Qy 485 GRP-----GDRRAEKGPAPKPTGOKWLLDIN-----QKSENPRDLFLNAVLONR 530
 Db 495 KRPKALKLLGMEDEPEPAKGGKKKKKKKEEIDIDVDDPAVSRRQYPPHELMNAVLMKR 554
 Qy 531 HEMATYFWANGQEGVAAALAAKILKEMSHLETEAANA-----RATREAKERYLALDLF 584
 Db 555 OKMAVFLMORGEESMAKALVACKLYKAMAHESSESDLVDDISQDLNNSKDFGQALLETLL 614
 Qy 585 SECYSNEBARFALLVNRNCWSKTTGLHATEADAFAFFHDGVAFLTIWNG--DMA 642
 Db 615 DQSYHDEQIAMKLLTYELKNWSNSTCLKLAVAKHDFIAHTCSQMLTMMNGRLMR 674
 Qy 643 AGTEILRLGAFLCFALVYTVTLITFSEEARPLRTGLEDLODSDLTESPLGLQSRVEE 702
 Db 675 KNPKLKYIMGLLPLEPTLPLEFRTY-----DDFSIQTSKENDGKEEEN 720
 Qy 703 L--VEAPRAQD-----RGRAVFLLTRMKFPGAVTYFLGNVNYFAFLPFTYVL 754
 Db 721 TDANADGSRKGDENEHKKORIPIGTKICKFYNAPIVKFWFTISIGVLLFNVTYL 780
 Qy 755 VDFRPPQGSQSPVTVYFNVFTVLEIRQGFETDTHLVKFTLYVGDNNKCDMVA 814
 Db 781 VRM---DQWPSLOEMIVISYIVSLALEKIRE-ILMSEPGKLSQKIKVWLOEYNNITDLVA 836
 Qy 815 IFLFTVCTCRMLPSAFEAGRTVLAQPMVFTLRLHHPAIHQDGPRIIVEHMMQOVF 874
 Db 837 ISTWIGAM-----ATRSVM-----NIGKMMIDML 861
 Qy 875 FFLFPLSVLVAVGVTTOALLPHDGRLEW-IFRRVLYRPLQIFGOIPLDEIDEARVNC 933
 Db 862 YFVIVMLVVLMSFCVAAQALHPEE-KPSWKLANIIFYMPWMLYGEVFDQID----- 914
 Qy 934 STHPLLEDSPSC-----BSLYANMVLILLTFLLVTVNLMLLIAMFSY 980
 Db 915 ---LYAMEINPPCCENLYDEBGRKLPPCIGAMCTPALMACYLLVANILLVNLIAVFNN 971
 Qy 981 TFOVQGNATMFMFORNYNIVEYHERPALAPRILLISHLSITLRV---FKSAEHRE 1037
 Db 972 TFEVKSISQWVKFYQYOLMTFHDRPLPPMILISHYITIMRISGRCKRKEGDOE 1031
 Qy 1038 HLERDL-----PPLDQKVVTWETVQKENFLSKMEKRRDSEGEVLRTAHRVDFIAKL 1092
 Db 1032 ERDGLKFLPSDEELKRLHEEEOCVQEHFREK-EDEQSSSDEIRITSRVENMRL 1090
 Qy 1093 GGLREOEK-----RIKLESQINYSVLVSSVADY-----LAQGGPRSSOHGE 1137
 Db 1091 EBNERTFPMKTSLOTVDRLAQLLEELSNRMVNALENLAGIDRSLIQARS-RASSEC-E 1148
 Qy 1138 GSQLVADHRGGIDGW 1153
 Db 1149 ATYLLROSSINSADGY 1164

RESULT 11

US-09-181-030-7
 ; Sequence 7, Application US/09181030
 ; Patent No. 6251597
 ; GENERAL INFORMATION:
 ; APPLICANT: Shyjan, Andrew W.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
 ; FILE REFERENCE: 07334/004005
 ; CURRENT APPLICATION NUMBER: US/09/181,030
 ; EARLIER FILING DATE: 1998-10-27
 ; EARLIER APPLICATION NUMBER: US 08/862,442
 ; EARLIER FILING DATE: 1997-05-23
 ; EARLIER APPLICATION NUMBER: US 08/623,679
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 7


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QY 318 FEQGSSELDVILKALYKACKSHSQEPDYLDELKLAVAMDRVIAKSEIFNGDVEW-- 375
DB 277 MGSEGOQDIEMALITLALKG--TNVSAP---DQSLALANRVDIASQIFVGPBHTP 330
QY 376 -----KSCD----- 379
DB 331 LGSILAPPTDSKATEKEKPRMATTKGRGKGGKGGKKEVEEBETDPKRIELLMVNA 390
QY 380 LEEVVDALVSNKPEFVRLFDNGADVADFLTYGRLOELYSRSKSLFDLORKOBEA 439
DB 391 LEQAMLDALVDRVDFVLLIENGVMQHFLITPRLEELYNTRLGPPNTLHLVADVKS 450
QY 440 RLTLAAGTQOARBPAPPAF--SLHEVSRLKDFLODAGR-----GFYOD 484
DB 451 NL-----PDYHISLIDIGLVEYLMGAVRCNTRKNFRTLYNNLGP 494
QY 485 GRP-----GDRRAEKGPAPKPTGQKMLDLN-----OKSENPRDLFLMVLQNR 530
DB 495 KRPKALKLGMEDDEPPAKGKKKKKKKEEIDIDVDPAVSRFQYPPELHMVMAVLMKR 554
QY 531 HEMATYFWMQGEVAAALAAACKILKEMSHLETEAEEA-----RATREAKYERLALDLF 584
DB 555 OKMAVFLMORGEESMAKALVACKLYKAMAHSSSDLDVDDISQDLNNSKDFGQALABEL 614
QY 585 SECYNSSEARAFALLVRRNRCSKTCTCLHATEADAKAFPAHDGVAFLTRIMWG--DMA 642
DB 645 DQSYGHDQIANKLLTYELKONMSNSTCLKLAVAAGHROFIANTCSQMLTDMNGRLMR 674
QY 643 AGTPLRLGAFLCALVYTNLITSEAPLRTGLEDLQDLSDLTEKSPLYGQSRVEE 702
DB 675 KNPGIKLVIMGILLPTIILFLEERTY-----DPSYOTSENEDEKKEEEN 720
QY 703 L---VEAPRAQD-----RGPRAVFLTRMRKFWGAPVTFNGVVMYFAFLFTTYVL 754
DB 721 TDANADASRKGBDENEHKQRIIPITGICKFVNAPIVKFMPYITISUGVILLNYYIL 780
QY 755 VDFRPPGPGSPEVTLFYWFVTLVEIRQGFPTDEBTHLVKKEFLYVGDMNKCMA 814
DB 781 VRM---DQMPSLQEWIVISYISLAKIRE--IMSEPGKLSQKIKWMLQEWNTITDLVA 836
QY 815 IFLFVGTCTMMLBSAFERGTVLAMDENVTLRLIHLFALHKQUGPKIIVERMKQVF 874
DB 837 ISTFMIGAM-----ATRSVM-----MIGKMMIDL 861
QY 875 FELFLSLVWLVAYGTTQALLHPHOGRLW--IFRVLVPRYIQIGQIPBDEIDARVNC 933
DB 862 YFVVMVLVMSFGVARQALHPBE--KPSWKLARNIFYMPYMWIYGEVFAQDID----- 914
QY 934 STHPLLEDSPSC-----PSLYANMLVILLVTLVTLVTLVTLVTLVTLVTLVTLV 980
DB 915 ---LYAMEINPCGENVLDEBGRKLRPCIPGAMVLPALMACYLLVANNILVNLVLAVERN 971
QY 981 TFOVQGNATMFWKFORYNLIVEYHERPALADPFIILSHLSTLLRV---FKKEAHEKRE 1037
DB 972 TEFVEKYSISNQWKFORYOLIMTFPHDRPVLPPMIIISHIYIIMRLSGRCKKEGDOE 1031
QY 1038 HLERL-----PDPIDQKVVTWETVQKENFLSKMKERRRDSGEVLRKTAHVDTIAKYL 1092
DB 1032 ERDRCLKFLSDEELKRLHFEBOQVOEHFRK--BDEQOSSSDERIRVTSSEVENMSML 1090
QY 1093 GGLREQEK-----RIKLESQINVCVLSVSVADV---LAOGGGRSSOHQGE 1137
DB 1091 BEINRETFPMKTSLOTVDRLRLAQLEELSNRMNALENLAGIDRSLQARS--RASSEC-E 1148
QY 1138 GSQLVADHRRGIDGM 1153
DB 1149 ATYLLRQSSINSADGY 1164

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RESULT 13
US-09-454-854-7
Sequence 7, Application US/09454854

```

; Patent No. 6316204
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
; TITLE OF INVENTION: AND TREATMENT OF TUMOR PROGRESSION
; FILE REFERENCE: 07334/004005
; CURRENT APPLICATION NUMBER: US/09/454, 854
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 09/181, 030
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 08/623, 679
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1497
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-454-854-7

Query Match 18.9%; Score 1150.5; DB 4; Length 1497;
Best Local Similarity 27.4%; Pred. No. 1.8e-103; Indels 275; Gaps 39;
Matches 349; Conservative 216; Mismatches 436;

QY 40 FVRVPSGVAPEVLDLLAEWHLPAPMLVSLVGEBOFPANKSWLRDYLKGLVQAOST 99
DB 2 YIRSYDTRKPSLSLHLWQKQWLEPKLLISVHGQNFEMQPKLVQVFGGLIKAAWTT 61
QY 100 GAWILTSALRYGLARHVGQAVRDSLASTSTKRVAVAGMASLGRVLRRLLEAODEF 158
DB 62 GAWIFGTGVSSTGVLSHWDALKDH---SSKSRGVCAIGIAPWGIIV-----EKEDLV 111
QY 159 ---PVHYPEDDGGSGPFLCSLDSNLSPHLYVEPPGPGDGLTELRLEKHSRO----- 211
DB 112 GKDVTRYVQYTNMSPNLSKLSVLSNTHFTILDNGLTKRYGAEVKLRLEHGISLQKINT 171
QY 212 RAGYGTGSIIEIPVLCILVNGDPNTERISRAVEOAPMLLV--GSGGIADVLA----- 264
DB 172 RLQGG-----VPLGLVVEGGPRVVSIVLELQEBPPIPVICDGSGRASDILSPAKY 225
QY 265 ---ALVNO---PHLYPKVAEKQFKEPKFSFMSWEDIVRWTKLONITSHQHLTYD 317
DB 226 CEEGIIINESLREOLLV--TIQTFNVYNAQSHOLFALIMECKM-----KKELVTVFR 276
QY 318 FEQGSSELDVILKALYKACKSHSQEPDYLDELKLAVAMDRVIAKSEIFNGDVEW-- 375
DB 277 MGSEGOQDIEMALITLALKG--TNVSAP---DQSLALANRVDIASQIFVGPBHTP 330
QY 376 -----KSCD----- 379
DB 331 LGSILAPPTDSKATEKEKPRMATTKGRGKGGKGGKKEVEEBETDPKRIELLMVNA 390
QY 380 LEEVVDALVSNKPEFVRLFDNGADVADFLTYGRLOELYSRSKSLFDLORKOBEA 439
DB 391 LEQAMLDALVDRVDFVLLIENGVMQHFLITPRLEELYNTRLGPPNTLHLVADVKS 450
QY 440 RLTLAAGTQOARBPAPPAF--SLHEVSRLKDFLODAGR-----GFYOD 484
DB 451 NL-----PDYHISLIDIGLVEYLMGAVRCNTRKNFRTLYNNLGP 494
QY 485 GRP-----GDRRAEKGPAPKPTGQKMLDLN-----OKSENPRDLFLMVLQNR 530
DB 495 KRPKALKLGMEDDEPPAKGKKKKKKKEEIDIDVDPAVSRFQYPPELHMVMAVLMKR 554
QY 531 HEMATYFWMQGEVAAALAAACKILKEMSHLETEAEEA-----RATREAKYERLALDLF 584
DB 555 OKMAVFLMORGEESMAKALVACKLYKAMAHSSSDLDVDDISQDLNNSKDFGQALABEL 614
QY 585 SECYNSSEARAFALLVRRNRCSKTCTCLHATEADAKAFPAHDGVAFLTRIMWG--DMA 642
DB 645 DQSYGHDQIANKLLTYELKONMSNSTCLKLAVAAGHROFIANTCSQMLTDMNGRLMR 674
QY 643 AGTPLRLGAFLCALVYTNLITSEAPLRTGLEDLQDLSDLTEKSPLYGQSRVEE 702

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Db      675 KNPGLKVMIGILLPPTILFLEFRTY-----DPSYQTSKXENEDGKEEBEN 720
Qy      703 L---VEAPRAGD-----RGPRAVFLTRMKFKMGAPVTVFIGNVVMYFAFLFTYVLL 754
Db      721 TDANDAGSRKGBDENENHKORIIPIGTICKCFYNAPIVKFWFYIISYGLYLLFNYYVL 780
Qy      755 VDFRPPQSGPEVTLFWVFTLVLEIRIOGFDEDETHLVKFKFLVYGDWNNKCDMVA 814
Db      781 VAM---DGMPSLOEMVIVISYVSLALEKIRE-ILMSEBGLSOKIKWLOEWMNTDLYA 836
Qy      815 IFLFVIGVTCRMLPSAFEGARTVLAMDPMVFTLRILHFAHKOLGPKIIVERMMKDV 874
Db      837 ISTFMIGAM-----ATRSVM-----MICKWMIDWL 861
Qy      875 FFLFLSLWLVAVGYTTQALLPHPHGRLEW-IFRRVLYRPYLOIRGOIPLDEIDARVNC 933
Db      862 YFVVIMLVLMSEFGVARQAIHPHEE-KPSMKLARNIFMPYMWYIGVEFADID----- 914
Qy      934 STHPILLDEDSPEC-----PSLYANMLVILLVTFPLVLTNTVNLMLLJAMFSY 980
Db      915 ---LYAMEINPPCGENLYDEBGRKLPCTPGAMLTALMACYLLVANILLVLLAVFN 971
Qy      981 TFOVVOGNATMFKFORVNLIVEYHERPALAPFILLSHLSLTLRRV---FKKEAHEKRE 1037
Db      972 TFEVYKSIISNQWVKFORQOLIMTFHDRVLPPLMIILSHIYIIMRLSGCRKKEGDOE 1031
Qy      1038 HLEBDL-----PDPDQKVVTWETVOKENFLSKMEKRRDSEGEVLRTAHVDFIAKYL 1092
Db      1032 ERDRGLKFLSDEELKRLHEFEQCQVQHFREK-EDBOOSSDERIRVTSERVENMSML 1090
Qy      1093 GGLREOEK-----RIKLESQIYVCSLVSSVADV---LAOGGPRSSOHCGE 1137
Db      1091 EGINERETMKTSLOQVDRILQLEBELSRMNALENLAGIDRSLLQARS-RASSEC-E 1148
Qy      1138 GSQVAAADHRGIDGW 1153
Db      1149 ATYLLRQSSINSADGV 1164

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RESULT 14
US-09-164-671-7
; Sequence 7, Application US/09164671A
; Patent No. 6372896
; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION
; FILE REFERENCE: 07334/004004
; CURRENT APPLICATION NUMBER: US/09/164,671A
; EARLIER APPLICATION NUMBER: US 08/862,442
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: US 08/623,679
; EARLIER FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FaastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 1497
; TYPE: PRN
; ORGANISM: Homo sapiens
US-09-164-671-7

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Query Match      18.9%; Score 1150.5; DB 4; Length 1497;
Best Local Similarity 27.4%; Pred. No. 1,8e-103;
Matches 349; Conservative 216; Mismatches 436; Indels 275; Gaps 39;

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Qy      40 FVRVPSGAVSVLFDLLABWMLPAPNLVVSILVGEOPAMSKWLDVLRKGLVKAQOST 99
Db      2 YIRVSDTTPDSILHLVMDOWLEPKLIISVHGCIQNFEMOPKLVQVGGKGLIKAMTT 61
Qy      100 GAMILTSALRVGLARHVGAVDRDHSLASTSTKRVAVAVGMAISGRVLAHRRILIEAQEDF- 158

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Db      62 GAMILFTGVTGIVSHVDAIKDH---SSKSRGRVCAIGAPMGIV-----ENKEDLV 111
Qy      159 ---PVHYEDDGGSGGCPCLSDSNLSHFLVEPPEPGKDDGLTELRLLEKHSIPO----- 211
Db      112 GKDVTRVYQTMSPNPSKLSVLNNSHTHFLDNGTLGKGAEVKRLLEKHSISQKINT 171
Qy      212 RAGYGTGSIIEIPVLCILVNDPPTLERISRAVEQAEMWLLV---GSGGIADVLA----- 264
Db      112 RLGGG-----VPLVGLVVEGGPNVSVILEYQGEPEPIPVICDGSGRASDIISFAHY 225
Qy      265 ---ALVNO---PHLVKRAVKQKFKFPSSKHSMEIVKTKLQNTISQHLTTYD 317
Db      226 CEEGGIINESREOLV---TIQTFNNYKAOSHOFATIMCMK-----KKELVTFR 276
Qy      318 FEOGSEELDTYILKALVAKCKSHSQEPQDYDELKLVANDRVDIASKEIFNGDVEN-- 375
Db      277 MGSEGOQDIEAAILTALIKG---TNVSAP---DQSLSLANRRVDIASQIFVFPHPHTP 330
Qy      376 -----KSCD----- 379
Db      331 LGSILAPPTDSKATEKEXKRPMAATTGGRGKGKGGKGVKEVEBEDTPRKIELLMVNA 390
Qy      380 LEEVWVDAIVSNKPEFVRLFVNDGADVADFLTYGRLOLYRSVSKSLPDLLOKQOSEA 439
Db      331 LEQAMLDAVLVDVDFVFKLLIENGVMQHFLTPRELIELYTRLGCPNTLHLVADVKS 450
Qy      440 RLTLAIGLQOAREBPAPAF--SLHEVSRLKFLQDACR-----GFYQD 484
Db      451 NL-----PDDYHSLIDIGLVELETMGATRCNTRKGRFRLYNNLFGP 494
Qy      485 GRP-----GDRRAEKGPAPKPTGQKMLLDLN-----OKSENPWRDLFLMAVLQNR 530
Db      495 KRPKALKULGMEDDEPPAKGKKKKKKKEEIDIVDDPAVSFRFQYPHELMVMAVLMKR 554
Qy      531 HEMATYFPAQGEVAAALLAACKILIKENSHLETEBA-----RATEAKYERLALDLF 584
Db      555 QMAVFLWQGBESMAKALVACKLYKMAHSSSESDLVDDISQDDINNSKDFGQALABEL 614
Qy      585 SECYNSBARAFALLVRNRCSKTTCHLATEADAKAFPAHDQVQAFLTRIMWG--DMA 642
Db      615 DQSYHDOIAMKLLTYELKWNNSSTCLKLVAAHGRPIAHTCQMLITDMMRRLMR 674
Qy      643 AGTPILRLGAFLCFALVYTNLIITPSEBAPRTGLEDDLODLSLDEKSPLYGLQRYEE 702
Db      675 KNPGLKVMIGILLPPTILFLEFRTY-----DPSYQTSKXENEDGKEEBEN 720
Qy      703 L---VEAPRAGD-----RGPRAVFLTRMKFKMGAPVTVFIGNVVMYFAFLFTYVLL 754
Db      721 TDANDAGSRKGBDENENHKORIIPIGTICKCFYNAPIVKFWFYIISYGLYLLFNYYVL 780
Qy      755 VDFRPPQSGPEVTLFWVFTLVLEIRIOGFDEDETHLVKFKFLVYGDWNNKCDMVA 814
Db      781 VAM---DGMPSLOEMVIVISYVSLALEKIRE-ILMSEBGLSOKIKWLOEWMNTDLYA 836
Qy      815 IFLFVIGVTCRMLPSAFEGARTVLAMDPMVFTLRILHFAHKOLGPKIIVERMMKDV 874
Db      837 ISTFMIGAM-----ATRSVM-----MICKWMIDWL 861
Qy      875 FFLFLSLWLVAVGYTTQALLPHPHGRLEW-IFRRVLYRPYLOIRGOIPLDEIDARVNC 933
Db      862 YFVVIMLVLMSEFGVARQAIHPHEE-KPSMKLARNIFMPYMWYIGVEFADID----- 914
Qy      934 STHPILLDEDSPEC-----PSLYANMLVILLVTFPLVLTNTVNLMLLJAMFSY 980
Db      915 ---LYAMEINPPCGENLYDEBGRKLPCTPGAMLTALMACYLLVANILLVLLAVFN 971
Qy      981 TFOVVOGNATMFKFORVNLIVEYHERPALAPFILLSHLSLTLRRV---FKKEAHEKRE 1037
Db      972 TFEVYKSIISNQWVKFORQOLIMTFHDRVLPPLMIILSHIYIIMRLSGCRKKEGDOE 1031
Qy      1038 HLEBDL-----PDPDQKVVTWETVOKENFLSKMEKRRDSEGEVLRTAHVDFIAKYL 1092
Db      1032 ERDRGLKFLSDEELKRLHEFEQCQVQHFREK-EDBOOSSDERIRVTSERVENMSML 1090

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Qy 1093 GGLREQEK-----RIKLESQINYSVLVSVADV----LAQGGGRSSQHCE 1137
Db 1091 EENIEREFEMKTSLOTVDRFLAQLEBELSRMVALENLAGIDRDLIDARS-RASSEC-E 1148
Qy 1138 GSQVLAADHRCIDGM 1153
Db 1149 ATYLLRQSSINSADGY 1164

RESULT 15

US-09-020-956-112
; Sequence 112, Application US/09020956
; Patent No. 6261562
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillin, Davin C.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO
; NUMBER OF SEQUENCES: 178
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,956
; FILING DATE: 09-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.427C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-09-020-956-112

Query Match 13.3%; Score 813; DB 3; Length 315;
Best Local Similarity 52.4%; Pred. No. 2.3e-71;
Matches 162; Conservative 53; Mismatches 68; Indels 26; Gaps 5;

Qy 843 MFTFLRLHIFPAIHKOLGKTIIVERMMKDVFFFLPFLSVMLVAGVTTQALIHPHDRL 902
Db 1 MFTVRLHIFVFNKQLGPKTIIVSKMKDVFFFLPFLGVLVAAGVATEGLRPRDSDF 60
Qy 903 EMIFRRVLVYRPIQIFGOIPLDEIDARV---NCSTHPLLEDSP-----SCPSLYANWL 954
Db 61 PSILARVYRPIQIFGOIPQEDMDVALMEHNSCSSEPGFMAHPGAQAGTCSQYANWL 120
Qy 955 VILLIVTLVTLVNLVLLIMFSTYTPQVVOGNAITMFKFORYNLIVEYHERPALADPF 1014
Db 121 VLLIVIFLIVANILLVNLIMFSTYTGKVOGNSDLWKQRYRLIREFHSRPAADPF 180
Qy 1015 ILLSHLSLTIRRVFK-----EASHKREHLERDLPLDQKVVTMETVQKENFLSK 1065
Db 181 IVISHRLRLRLKOLCRPPSPQSPSPALBHFVYLSKE---AERKLTWESVHKENFLLA 236

Qy 1066 MEKRRDSEGEVLKRTAHVDFIAKYIGLREQEKRIKLESQINYSVLVSVADVILAQ 1125
Db 237 RARDKRESDSERLKRSTOKVDLALKOLGHIREFQRILKVLIEREVQOCSRVLGWVAEALSR 296
Qy 1126 G-----GGP 1129
Db 297 SALLPFGGP 305

Search completed: September 10, 2003, 09:42:29
Job time : 27 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: September 10, 2003, 09:30:54 ; Search time 27 Seconds
(without alignments)
4149.501 Million cell updates/sec

Title: US-09-834-792C-4
Perfect score: 6051
Sequence: 1 MODVQGPSPGDAEDRR.....HRGGIDGWEQPGAGPSPDT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:
2: pir2:
3: pir3:
4: pir4:

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1058.5	17.4	1868	2 T23707	hypothetical prote
2	990	16.3	1400	2 T22644	hypothetical prote
3	881	14.5	1707	2 T18951	hypothetical prote
4	319.5	5.2	1275	2 JN0092	trp protein - fruit
5	310.5	5.1	1274	2 JN0015	trp protein - fruit
6	290	4.8	1418	2 S40764	hypothetical prote
7	262.5	4.3	1124	2 JH0588	calmodulin-binding
8	239	3.9	899	2 F88391	protein R06B10.4
9	234.5	3.8	823	2 S44873	ZC21.2 protein - C
10	186	3.1	828	2 UC5807	trp3 protein - rat
11	170.5	2.8	793	2 S68238	trp-1 protein - hu
12	170.5	2.8	810	2 I38361	TRP1 protein - hu
13	166	2.7	823	2 T34472	hypothetical prote
14	164.5	2.7	3678	2 S28916	hypothetical prote
15	153.5	2.5	482	2 S61648	dyserophin - mouse
16	142	2.3	839	2 UC7621	probable membrane
17	140.5	2.3	675	2 T20822	capsaicin receptor
18	139	2.3	725	2 JC7531	calcium transport
19	138	2.3	900	2 T33026	hypothetical prote
20	135	2.2	790	2 T20312	hypothetical prote
21	132	2.2	727	2 UC7796	epithelial calcium
22	127	2.1	2049	2 T43161	sodium channel pro
23	125.5	2.1	2322	2 T10542	hypothetical prote
24	125	2.1	838	2 T09054	capsaicin receptor
25	123	2.0	1060	2 S63993	hypothetical prote
26	123	2.0	1075	2 T45570	kinasin-like prote
27	123	2.0	2206	2 JC5280	voltage-dependent
28	122.5	2.0	1199	2 T37561	probable transcrip
29	122.5	2.0	3685	1 A27605	dyserophin, muscic

30	122	2.0	723	2 UC7795	epithelial calcium
31	121.5	2.0	608	2 G02640	polycystic kidney
32	121.5	2.0	2388	2 JB0271	beta spectrin, bet
33	121	2.0	1657	2 T15838	hypothetical prote
34	120.5	2.0	1506	2 S52957	bind protein - Eme
35	120	2.0	2019	2 A33996	sodium channel pro
36	120	2.0	5149	2 F83345	probable non-ribos
37	119.5	2.0	1559	2 T30535	calcium channel al
38	119	2.0	937	2 T37241	olfactory channel
39	118.5	1.9	2472	2 A35715	fodrin alpha chain
40	118	1.9	1951	2 S00320	sodium channel pro
41	118	1.9	1983	2 A60054	sodium channel pro
42	117.5	1.9	854	2 T23155	hypothetical prote
43	117	1.9	957	2 D88651	protein B0212.5
44	116.5	1.9	1687	2 S41742	calcium channel al
45	116	1.9	638	2 UC7753	ring finger B-box

ALIGNMENTS

RESULT 1
T23707
hypothetical protein T01H8.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C:Accession: T23707; T24342
R:Kershaw, J. the EMBL Data Library, November 1996
Submitted to the EMBL Data Library, November 1996
A:Reference number: Z19786
A:Accession: T23707
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1868 <W12>
A:Cross-references: EMBL:Z80219; PIDN:CA805572.1; GSPDB:GNO0019; CESP:T01H8.5
A:Experimental source: clone M04C7
R:Lenhard, N.
Submitted to the EMBL Data Library, September 1996
A:Reference number: Z19877
A:Accession: T24342
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1868 <W12>
A:Cross-references: EMBL:Z80219; PIDN:CA802303.1; GSPDB:GNO0019; CESP:T01H8.5
A:Experimental source: clone T01H8
C:Genetics:
A:Gene: CESP:T01H8.5
A:Map position: 1
A:introns: 24/3; 112/3; 191/3; 220/1; 268/2; 375/2; 456/2; 552/3; 625/2; 744/3; 850/2; 1

Query Match 17.4%; Score 1058.5; DB 2; Length 1868;
Best Local Similarity 24.4%; Pred. No. 5.5e-68;
Matches 342; Conservative 231; Mismatches 487; Indels 341; Gaps 41;

26 GEVNF-GSGKKRGKGVVPSGVA SVFLDLAEWHPAPNLVSLVGEOPFAMKSM 84
214 GQVEFGSPHYKQYRVNFDTEPAYIMSLFENWQSPRLIITVVGSGNSFDLQKL 273
85 RDVLRKGLVKAAGSTGAWILTSALRVGLARHVGAVDRDHSIAGTSTKYRVAVAGMAGSLGR 144
274 ARVRKRGILLKAASITGAMIITSGCDTGVAKHVAALLEG---AQSAQRKKVICIGIAPWG- 329
145 VLHRRILEAEQEDF-----FVHVPEDDGSQGLCSLSLSLSPFIIVERPPGKGDLLT 198
330 -----LTKKREDITGQDKTVPYVP--SSSKGFTGLNNHSHYFLVDNGTVGGYGAEV 380
199 ELRLRLKRLKHSIQAGYGTGSIIRIPVLCILVNDPMTLERISRVADEQA--APMLILVGS 256
381 ILRRLRLKRLKHSIQAGYGTGSIIRIPVLCILVNDPMTLERISRVADEQA--APMLILVGS 438
257 GGIDVTLAAL--VNQPHLL-----VPKVAEKQFKPKSPKSPFMSWEDIVRMKTLONT 306
439 GRADLLAFAHQNTEDGLLEPDDIRROVLLIVETTFGCSSEAAAH-----RLHHEL 488

Qy	307	T---	SHOHLTVNDEOGSEBEPVILKIAVKACKSHSOBPODYDEBKIAVMDRVDI	363
Db	489	TVCAQHKKLLTIFRLGEGEHVDVDAIITALKG----	ONLSAODQALALAMNRDI	542
Qy	364	AKSEIFNDVBMKSCDLEEVNVDALVSKPEFVRFLVNGADVADFTLGYHLOELY----		419
Db	543	ARSDVFAHGHMPCQAALNNAMMEALIHVRDVFRLLEOGINOKFKLTISLDELYNTDK		602
Qy	420	-----RSVSRK-----SLFPDL-----	ORKOEARL	441
Db	603	GPPTLTIFYIVADVVRROGYRFPKLPDGLVETIEKMGNSGYCSYTTSEPRDKYKORMKRVK		662
Qy	442	-----TLAGLGTQOAR-----	PPAGPRA-F	461
Db	663	HAOKKMGVFSRRPSRTSGIASRSTGCMGVGSSVAGVFGNSFGNODPPLDPHYNR		722
Qy	462	SLHEYSRLXKPLF--ODACRGFYODGRBGDRBRAAKGPAKPGTQOKWLLDINOKSEN----		516
Db	723	SALSGSRPLSNHILMRSAFGRNF-----PANPMRPNLGDSPDCSGEPFEEELSTLSASGCS		778
Qy	517	-----PMBDPLMAVLQNRHEMATYFMAMGEGVAAALAAKILKEMS-----HLE		562
Db	779	QTEPDPFRPYSELMIWAVLTRQDWMQCMQGHGEAMAKALVACRLYKSLATEAEDYLE		838
Qy	563	TEABAPARTBAKTERLALDFSEBCYSSEAPAFALLVRRNRCSKTTCLHLATEADAKA		622
Db	839	VEIGEBELKKVABEERFLSLLELHDHCYHDDAQOTLTLTYELSNMNETCICALAVIVANKH		898
Qy	623	FPAMDGVCAFTRIMXGMAAGT-PIALMLAFLICFALV-----		660
Db	899	FLAHPCCOILLADLHGGRLMRHTSNITVVGILCIPPTIOMLEBKTEBELLNOPATAEH		958
Qy	661	-----YTMLITFSEBAPLRTGLELDLODLSIDTE-----		689
Db	959	QNDMNYSSESSSSSSSSSSSSSSSSSPEDDENNANHQOKRTRKTSQGSAGSLNITS		1018
Qy	690	-----		689
Db	1019	LPHSRRRKAKKNEKCDRETDASACENGRQIONGGLTAEYGTFGESNGSVSPPPYMRANS		1078
Qy	690	-----KSPGLGQSRVEIYEAAPRAQDR-----	GPRAVFLTRMRKFW	728
Db	1079	RSRYNNSDMGKTSVITGSPDNLSKQKSNITSTDRNPMEOGQTRKIKIMRRRFFEFY		1138
Qy	729	GAPYTVFLGNVVMYAPFLFTFYVLLVDFRPPPOGSGPEVTILYFWFTVLEEROGFF		788
Db	1139	SAPISTFMSWMTISFLFTFTFTYLLV--KTPPR-PIYIEKILAYAAPELGEVQRKIM		1195
Qy	789	TDEBTHLVKKFTLYVGDWNKCDMAVFLFTIVGYTCRMLPSAFAEGRTVLAJMDFMVFTLR		848
Db	1196	SDAPR-FYEKIRTYVCSFWNCVTJLAIIFYIIVGFPMRCFGSV-ANGRVILACDSVLMWMK		1253
Qy	849	LIHIFAIHKQGPRTKIVVERMKKVFFFLFSLVWLVAYGYTTQALLHPHGRLEWTF-R		907
Db	1254	LDDVMSVHPKPGPYTAGKMIQNNXYIWMVLVYTLISFGLAROSITYP-DETHWMLIVR		1312
Qy	908	RVLVRPYQIIFGOJPLDEIDEARVNCSTH-----	PLLEDSF---SCPSLVAWML	954
Db	1313	NIFLKPYPMLGVEYADEID-----TCGBEAMDQHLENGCPVILGNTTGSLSCVGEY-WI		1366
Qy	955	VILLVTEFLVTVNLVNLMLIAMSYYTPQVQVGNATMFWKFORYNLIVYEHBRPALAPF		1014
Db	1367	PPLMTTFELLANILMMLAIIFNHIFDADIDEMSGQIWLFORXYQVWEVESTFPLRPL		1426
Qy	1015	ILLSHLSTLTRVFKKEAEKREH-----	LERDLPPDLQKVNTWETVQKENTL-S	1064
Db	1427	TPLYUGVILITQFVVRTRLSCSKSOERNPILIKIAELFDNQIOIKLHDFEEDCMEDUARQ		1486
Qy	1065	KMEKRRRPSSEGVAKTAKHR-----	VDFLAKYLG---LRDEKRIKCLSEQIYNCSV	1114
Db	1487	KLEKNNTSNEGRILKADIRTOQILNRLDLOAKESMGADVINDVESRLASVEKQON--E		1543

RESULT 2
T22644

hypothetical protein F54D1.5 - Caenorhabditis elegans
C1Species: Caenorhabditis elegans
C1Date: 15-Oct-1999 #sequence_Revision 15-Oct-1999 #text_change 15-Oct-1999
C1Accession: T22644
R:Lennard, N.
submitted to the EMBL Data Library, July 1996
A:Reference number: Z19592
A:Accession: T22644
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1400 <MIL>
A:Cross-references: EMBL:Z77132; PIDN:CA800861.1; GSPDB:GN00022; CESP:F54D1.5
A:Experimental source: clone F54D1
A:Genetic8:
A:Gene: CESP:F54D1.5
A:Map position: 4
A:introns: 21/2; 51/2; 205/2; 276/3; 364/2; 466/3; 507/3; 536/3; 599/3; 672/2; 691/2

Query Match 16.3% Score 990: DB 2: Length 1400:

Best Local Similarity 27.7%; Pred. No. 3.4e-63;

Matches 334; Conservative 202; Mismatches 401; Indels 188; Gaps 46;

Db 151 GTITFGGGAHAKKQVYRLSYDESEPLDVIMTEKWGLBAPRLVITVHGCMNFELBERL 210

Oy 26 GEVNF--GGSGKKRGKFRVPVPSGVAHSVLPDLLAEMLPAPNLVSLVGGEOPFAMKSWL 84

Db 151 GTITFGGGAHAKKQVYRLSYDESEPLDVIMTEKWGLBAPRLVITVHGCMNFELBERL 210

Oy 85 RDVIRKRLVLAAGSTGMILTSLRVGLAHNVQAVDHSLASTSKVRVAVAGMASLGR 144

Db 211 GRLEPRKMMLRAAQTTGAMITTSGLDSGVHVAAAL--DEAGISARMSQSIVTTIGIAPWG 269

Oy 145 VLAHRRIIEAEOEDPVHYRPDDGSGOPLCSLDLSNLSHFLIVERGPCKDGTELRLRL 204

Db 270 IKKERIRLRONEH--VYYDVHSLSVNANVGILMDRHSYFLIADNGTVGRGADLIHQNL 327

Oy 205 EKHISEOPAGYGGTGSIETIPVLCLLVNGDPNTLERISRAY--EQAAFILLVSGGIADV 262

Db 328 ENHI-----ATFGCGNGR-KVPPVCTLLLEGSSISINAIHDVYTMKPDIPIAVCDGSGRAADI 382

Oy 263 L---AALVNPCHLLVPRVAEK---QEKEKPPSKHFSMEDIVRMTKLIQNTSHQHLLTY 316

Db 383 ISPARAYINDGTFPAAVGEGKLRLNIIMVEPER--DOEWMFR--KITECVI-RDDLRLIF 437

Oy 317 DFEQGSGEELDTVLKALVLRACKSHSQEPDYLDELKLAAMRDVIDAKSEIFNGVEMW 376

Db 438 RYQGEEBEDVDVFLISTVLQ----KNLPPD--EQALLTSMWRVLDLAKSCFLPSNGRKMS 491

Oy 377 SCDLIEVMVALVSNNKEPFYRLFPVNDGADVAADFITYGRLOELY-----RSYSRKSLL 428

Db 492 SDVLEKAMNDALYMDRVDFECLLENGVSKMFESIIRLTENLYMMDINSASHSVRYNMEN 551

Oy 429 FDLLIQROEABRLTLAAGTQQAAREPPAGPAPSLHVSFVULDFQLDACRGFYQDGRPG 488

Db 552 FDSN--DPHTYLLTPMITG--QVEVKLMG-NAPQLYTTSRKF-----GKYD 592

Oy 489 DRRAERKCP---AKRPFGQKMLL-----DLNQKSEN-----PWRLFTMAVLONRHEN 533

Db 593 RYKRINGSYFHRRRKTIYQKELFFPKKSDQGINNEBEDSFAPVPFNLLIMAVLTSHGMM 652

Oy 534 ATTFWAMGQGVAAALAACKILK-----EMSHLETAEARATRREA-KTERLALDLFSE 586

Db 653 AECMWVAVGEBAAMAKCLIAIRLYKATAKIADDEVLYDVE-EAKRFLDNVAKCREDAIBELDQ 711

Oy 587 CYNSEBARAFALLVRRNRCKSKTTCCHLAILEADAQKAFADVGQAFTRITMWDQM--AAG 644

Db 712 CYRADHDRTRLRLMEILPHMGNNNCUSLAYLANIKTFLAHPCCOILLAEIMHSGSLKVRSG 771

Qy 645 TPPIRLGAFIC---PALVY-----TNLITPSEBAPLRTGLEDI-QDLSLDTEKSPLY 694
 Db 772 SNV-RVLTAALICPPAILFMAYKPKHAKTARLSEETP-----EQLPYRESITSTTSNR 825
 Qy 695 GLGQREVELVEAPRAQG-----DRGPAVE-----LITPRK 726
 Db 826 RYSGPBEQKTLLEKGSYTKKVTIISRRKNSGVASVGSASSMFKPEPOLANKFERRA 885
 Qy 727 FWCAPVTVFLGNVVMYFAFLFTYVLLVDRPPQGSREVTLYFWVFTLVLEIRG 786
 Db 886 FYSSPITKFMSCWICAFILFTTCICILFE---TSKSKYEMITFIYTVLSVHIRK- 941
 Qy 942 LMTSEGSINEKVKVFKYAKWNIMTSALLFELVGYGRFLVPMYRHSNGRVLSPNVLF 1001
 Db 846 TLRILHFAIKQCPKIIIVERMMKDVFFFLFPLSVLVAVGTTQALLPHRGRLEWI 905
 Qy 1002 YMKLFEYLVHPPLGPIYQMAKAVMSVCYICVLLVPLMAFGVNRQALTEPNYKDMWL 1061
 Qy 906 F-REVLRYPIQIFGOIPLDEIDEARVNCSTHPLLEDSPCSPSLYANWVILLVFL 964
 Db 1062 LVRIHIFKPYFMYLGEVYAGEID-----TCG-----DEGICPGFY--FIRPLMVFIL 1109
 Qy 965 VTVALNMLLIAMFSYTFQVVGNAFMFKQRYNLIVYHERPALAPFILLSHL----- 1020
 Db 1110 VANILLNMLLIAMFSYTFQVVGNAFMFKQRYNLIVYHERPALAPFILLSHL----- 1169
 Qy 1021 --SLTLRVRFK-----EAEHR-EHLERLPPLOKVTTWTVQKENPLS 1064
 Db 1170 DYLNLRPDPTRPRSEHSIKLSTVEDMKRIODEEDCIDTLTR-----IRK---L 1218
 Qy 1065 KMEKRRDSEGEVLRTAHRY-----DFIAKYLGLEGEKRIKCSQINYSVLVSS 1118
 Db 1219 KLNKPEPLSVTDLELTCQRVHDMQENFLK-----SRVYDIETKIDHINSNDE 1269
 Qy 1119 VADV 1123
 Db 1270 VQVIL 1274

RESULT 3

T18951
 hypochetrical protein C05C12.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T18951
 R:White, S.
 submitted to the EMBL Data Library, January 1996
 A:Reference number: Z19050
 A:Accession: T18951
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1707 <MW>
 A:Cross-references: EMBL:Z68333, PIDN:CAA92726.1, GSPDB:GN00022, CESP:C05C12.3
 A:Experimental source: clone C05C12
 C:Genetics:
 A:Gene: CESP:C05C12.3
 A:Map position: 4
 A:Introns: 13/3; 52/3; 82/3; 100/3; 174/3; 203/1; 249/2; 292/1; 358/2; 406/2; 436/2; 477/2
 542/3; 1595/1; 1647/2; 1673/3; 1695/3

Query March 14.5%; Score 881; DB 2; Length 1707;
 Best Local Similarity 22.2%; Pred. No. 3.8e-55;
 Matches 306; Conservative 227; Mismatches 465; Indels 380; Gaps 41;

Qy 26 GEVNFSGGKRRGKRVVPVSGVAPSVLEFDLLAEWHLPAPIVLVSLVGEOPFAMKSWLR 85
 Db 197 GNIVFEGTA-HHAQYARISFDSPPRDIVHLMMKWKLPKLIITINGLTKFLDQPLTA 255
 Qy 86 DVLRKGLVKAQSGAWITLTSALRVGLARHGOAVRDSLASTSTKRVAVAVGASAGRV 145
 Db 256 RTFRKGIKIAKSTDAWITITGLDEGVVGLHDSALHDI--GNHTSKHVAIVAGIASWGML 313

Qy 146 LHRRIIEAOEDPEVHYPEDDGSQGLCSLDSNLSHFIIIVEPPEPKGDELTELRLLE 205
 Db 314 KQRS-RFVGKDSVTYATATVFNNT-RLKELNDHSHFLPSDNQTVRYGAEIIMRRBLE 370
 Qy 206 KHISEQAGYGGTSGIIEIPVLCILVNDPNTLERISPAVE--QAAPVLIVSGGIADVL 263
 Db 371 AYLAQ-----GDKKRSALPLVCVLEGAFTIKVHVHYVTTPRIPIVICGSGRADIL 425
 Qy 264 A-----ALVNPCHLV---PVAEKQREKRPKSGHFSMEDLVRTKL 302
 Db 426 AFAHQAVSNGFLSDNIRNQLVNIVRRIFGYDPTAKLILKQ----- 467
 Qy 303 LQNTSHQHLITVYDFQESSELDVTIILKALYKACSHSOEPQDYLDELTAVAMPVD 362
 Db 468 IVECTNKSMTIIRLGESSREDIDHYMCL--KGOMLSP--EQDOLALANRAD 521
 Qy 363 IAKSEIFNGDVKSCDLEEVMDALVSNKPEFVRLFVNDGADVADELTYGRLOELY-- 419
 Db 522 IARTEIPANGTEWTTQDLNHNAMTEALSNDRIDFVHLLENGVSQKFLTYGRLEHLYNTD 581
 Qy 420 ---RSVRSKSLPDLQKQBEARLTLAGLCTQARPPAPRPAFSLHVSRYLKDPLQD 476
 Db 582 KGPQNTLRNLVDSKIH-----IKLVEGRIVENLMGN 615
 Qy 477 ACRGFYOD-----GRPDRRRAEK----- 495
 Db 616 LYKSNYTKFEKQYQYFLFNRRKQGRKRVHNSNGRNDVIGSPSDAGREKMSQISLIN 675
 Qy 496 -----GPAKPTQOKMLLDLNKSEN-----PWRDLFMAVLONHEMATY 536
 Db 676 NARNSIISLFGNGGRKRESDDEDPSNLEEEANMDFRYPYSDLMIAVLTKQOKAKL 735
 Qy 537 FPMAGGVAAALAAKILKEMSHLTEAPAAATRA-----KYERLALDFS 585
 Db 736 MWHGEEGMKALVASHL-----YVSLAKTASLATGIGMSODETFESSDESELAVLE 790
 Qy 586 ECVNSBARAFALLVRNRCMSKTTCHLATEADAKAFPAHDGVAQLTRIMGDM----- 641
 Db 791 YCTHGRDQTLRLITTCGLANMGDETCLSLAANNCHRFLLHPPCCOMLLSDLMOGGLMKN 850
 Qy 642 -----AAGTPILRLGAFICFALVYTNLITPSEBAPLR-----TGLEDLQ 681
 Db 851 NQNSKVLTCLAAPPLIFLIGFTKEQMLPKTAABHDEBMSBEMKASBEDTDTSSSS 910
 Qy 682 DLDSLDL-----KSPVLGLQREVELVAP----- 707
 Db 911 DSDSDDEDAKLRAOSLSADQPLSIHRLVRDKLNFSEKKKPDWG---ISRIVVAPPIVT 966
 Qy 708 ---RAQ----- 710
 Db 967 GRNBARMTSIKSKKNVKKPACIKIETSDDEQOKKATEMCKSTFFDFPFPPIYNT 1026
 Qy 711 GDRGPRAV-----FLITR-----NRK---F 727
 Db 1027 GKGSVAVANNDMDYIDPSEELDTQRRKSRSEFSSRRVTVQVYQRLSMKKIMEF 1086
 Qy 728 WCAPVTVFLGNVVMYFA--FLEFITYVLLVDRPPQGSREVTLYFWVFTLVLE-- 781
 Db 1087 YKAPITTYW---LWFAFIWELILLTYNLVKTQ---RIASWSWYVFAIYFVTTLEIGR 1140
 Qy 782 EIRGFFTEDTHLVKKFETLYVGDNNMKCDMVAIFLIVGTCRMLPSAEAGTVALMD 841
 Db 1141 KVSTIMMDSKVYLKQLRVFPQYRNGLAFLGLIYLIYFIRLSFTTTLGHLITLIGN 1200
 Qy 842 FWFETTLIHFALIKQCPKIIIVERMMKDVFFFLFPLSVLVAVGTTQALLPHRGR 901
 Db 1201 SVIWSLKLTVYLSVQGLGPIYINIVAMIPMLPLCVLVPITLYAFGLAQSIYVYE-- 1258
 Qy 902 LEW---IFRVLVTRPIQIFGOIPLDEIDEARVNCSTHPLLEDSPCSPSLYAN----- 952
 Db 1259 -DWHMILVRNIPLQPYFMYLGEVYAGEID-----TCGDEIWTQHEDENIPISMNLVTHETC 1313

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QY 953 ----WLVIILVTFLVTNVLNMLLIMPSYTFQV-VQGNATMFKFORVNLIVEYER 1007
DB 1314 VEGWIAPGLTVMALNVLNMLNVAAGCTTIFEKHIOSTREIF-LERVQVWEIEST 1372
QY 1008 PALAPFLLSHSLTLRRVFKKEAEHKREHL-ERDL-----PDLQKQVVTWETQKEN 1061
DB 1373 PALPPFTIIVHVMLEFKIKSSRMFKRNLPDQSLKFLSPDPM-EKVHTFEESVED 1431
QY 1062 FLSKNEKRRRDEGEVLRTAHRVPFIKYLGL-----REDEKRIKCLSEQ 1108
DB 1432 MKRETEKKNLSSNDRIRHTARTDALNRSVHLTQLEFTLKEIRELEHKKNMDSR 1489

RESULT 4
trp protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 17-Nov-2000
C:Accession: J00092
R:Montell, C.; Rubin, G.M.
Neuron 2, 1313-1323, 1989
A:Title: Molecular characterization of the Drosophila trp locus: a putative integral mem
A:Reference number: J00092; MUID:90180449; PMID:2516726
A:Accession: J00092
A:Molecule type: mRNA
A:Residues: 1-1275 <MON>
A:Experimental source: strain Oregon R
C:Comment: trp protein is expressed predominantly in the rhabdomic membranes of the ph
A:Gene: trp
A:Cross-references: FlyBase:FBgn0003861
C:Superfamily: TRPC3 protein
C:Keywords: transmembrane protein
F:334-354/Domain: transmembrane #status predicted <TM1>
F:378-401/Domain: transmembrane #status predicted <TM2>
F:419-436/Domain: transmembrane #status predicted <TM3>
F:457-471/Domain: transmembrane #status predicted <TM4>
F:504-527/Domain: transmembrane #status predicted <TM5>
F:612-630/Domain: transmembrane #status predicted <TM6>
F:636-661/Domain: transmembrane #status predicted <TM7>

Query Match 5.2%; Score 319.5; DB 2; Length 1275;
Best Local Similarity 20.2%; Pred. No. 1.6e-14;
Matches 177; Conservative 123; Mismatches 265; Indels 313; Gaps 37;

QY 305 NITSHOHLITVDFEQQSGBELDTVLKLVKACKSHSQEPDYLDELKLAAMDRAVDIA 364
DB 86 NVLLLEHNIIEVGDLALHAISEEYEAIVEELQWEEFNHKGOPY-----SWEAVDRS 137
QY 365 KSEIFNGDVEMKSCDLEWVVDALVSNKPEFVRLPFVNDG-----DV 406
DB 138 KS-TFVVDI-----TPLLAHRNNYEILKILDRGTLMPHDVKGCCDECVTSQT 188
QY 407 ADFLTGRLQ-ELYRSVSRKSLFDLLQKQEBARLTLAGLGTQARBPAPGPAFSLH- 464
DB 189 TDSLRHSQSRINRYALSSSL-----ALSRDPVL-TAQQLSW 227
QY 465 EVSRVLKDLQDQCRGFDGPRGRRRAEKGPAPKPTGQKLLDLNQSSENPWRLFLW 524
DB 228 ELKRL--QAMESEFRREYTEMR---QWVDFGTS-----LIDHARTS-----MELE 268
QY 525 AVIQNHHEMATYFWANGQGEVAAALAAKLIKEMSHLETAEAARATREKRYERLALDLF 584
DB 269 VMLNFNHPESHDIWCLGQ-----RQTLER----- 292
QY 585 SECYSNSEARAFALLVRNRCMSKTCIHLATEADAKAFPAHDGVOAFLTRIMWGMMAAG 644
DB 293 -----LKAIRYKQKTFPAHNVOQLALAIYVD-----G 321
QY 645 TPILRLGAFLCFALVYTNLITSEAPLRTGLELDLDDLSLDTESPLYGLQSRVEELV 704
DB 322 LPGR-----RKQASQQLMDVVKLGC-SPIYVSL-----KYI 352

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QY 705 EAPRQGRGPRAVFLLTRMKFMGAPVTVFLGNVVMYFAFLFL----- 748
DB 353 LAPSEG-----AKFMKRPVFKITHSQYMFILMGAASLRVQITFELL 399
QY 749 -FTYVL-LVDFRPPQG--PSGPEVTLFVNFVLVLEIR-----QGFEDBDHLYKFF 799
DB 400 AFPMMLTLEDMRGKRGERSLPGPIELAIITYMALIFEELKSLYSDGLF----- 449
QY 800 TLVYGDMMNKCDMAVFLFIVGVTCR-----MLPS 829
DB 450 --YIMDLNINVDIYSNMFYVWILCRATAWIVYRDLMFRGIDYFREHHNPPDPMLLS 507
QY 830 --AEAGRTVLAMDPMVET-LRLIHFAIHQGLCPKIIIVERMKVDFFFLPFLSWLVA 886
DB 508 EGAFPAAG-----MVSYLKLVHIFISINPHLGLQVSLGRMIIIDIKFFFIYTLVLA 559
QY 887 YGVTTQALL-----HPHDGRLEW-----IFRRV-LYRP-----YLQIFGQ 920
DB 560 FGCGLMQLMYYAELEKKCYHLHPDVADFDQERACTIWRFSNLFETSQSLFWASFGL 619
QY 921 IPLDEIDARVNCSTHPLLEDSPSCPSLVANMWLILTLVTLVTVNVLNMLLIMPSY 980
DB 620 VDLVSFDLAGKS-----FTRFALLMFGSYVINIIVLNLMLIMMSN 663
QY 981 TFOVVOGNATMFKFORVNLIVEYHE-RPALAPFLLSHSLTLRRVFKKEAEHKREHL 1039
DB 664 SYQIISERADTEWFKARASQLMWSYFEDCGTLPPEPNCIPNNKMKRLTGRKPSRTKSF 723
QY 1040 ERDL-PPPLDQKVTWETQKENFLSMKRRDSEG 1075
DB 724 RKSMEARQTLHDKVM---KLVRRYIT-AEORRRDYG 757

RESULT 5
trp protein - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 02-Feb-2001
C:Accession: JN0015
R:Hong, F.; Schaefer, E.L.; Roop, B.C.; Lamendola, J.N.; Johnson-Seaton, D.; Shao, D.
Neuron 3, 81-94, 1989
A:Title: Proper function of the Drosophila trp gene product during pupal development is
A:Reference number: JN0015; MUID:90148782; PMID:2482778
A:Accession: JN0015
A:Molecule type: mRNA
A:Residues: 1-1274 <MON>
A:Comment: This photoreceptor membrane-associated protein is not required for the occur
A:Gene: trp
A:Cross-references: FlyBase:FBgn0003861
A:Map position: 99C5-6
C:Superfamily: TRPC3 protein
C:Keywords: glycoprotein; nucleotide binding; P-loop; phosphoprotein; transmembrane prot
F:1257-1263/Region: nucleotide-binding motif A (P-loop) #status predicted
F:64-70/Binding site: carbonyldiurate (Asn) (covalent) #status predicted
F:191,602,880,883,924/Binding site: phosphate (Ser) (covalent) #status predicted
F:800,1266/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 5.1%; Score 310.5; DB 2; Length 1274;
Best Local Similarity 20.2%; Pred. No. 7.4e-14;
Matches 186; Conservative 132; Mismatches 274; Indels 327; Gaps 41;

QY 274 VPKVLEK-QFKRPSKHSWEDIYRMKRLQNLNTH-----OHLTVYDFEQSGS 323
DB 48 VKKILSEYQGTDF--NINCTDPMKRSALISAENENFDMLVILHNIEVGDLALHAI 104
QY 324 EELDTVILKALVACKSHSQEPDYLDELKLAAMDRAVDIAKSEIFNGDVEMKSCDLEEV 383
DB 105 SEEYEAIVEELLQWEEFNHKGOPY-----SWEAVDRSKS-TFVVDITF----- 147
QY 384 MVDALVSNKPEFVRLPFVNDG-----DVADFLTGRLQ-ELYRSVSR 424
DB 148 LILAAHRNNYEILKILDRGATLMPHDVKGCCDECVTSQTTDSLRHSQSRINAYRALSA 207

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Db 970 QYANSPSCPS--OSLPAYLIVIEFVILKLLWPLIFAFPSKTAKNVDEADKIRFQLYS 1027

QY 1000 LIVEYHERPALAPPFL 1016

Db 1028 LAEDFRLRPLPPPLTI 1044

RESULT 7

JH0588

calmodulin-binding protein trpl - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 01-Mar-2002

C:Accession: JH0588

R:Phillips, A.M.; Bull, A.; Kelly, L.E.

Neuron 8, 631-642, 1992

A:Title: Identification of a Drosophila gene encoding a calmodulin-binding protein with

A:Reference number: JH0588; MID:92232293; PMID:1314616

A:Accession: JH0588

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1124 <PRT>

A:Cross-references: GB:M88185; MID:9469057; PID:q158715

A:Experimental source: head

C:Genetics:

A:Gene: trpl

A:Cross-references: FlyBase:FBgn0005614

C:Superfamily: TRPC3 protein

C:Keywords: calmodulin binding; phosphoprotein; transmembrane protein

F:3741-362/Domain: transmembrane #status predicted <TM1>

F:3741-396/Domain: transmembrane #status predicted <TM2>

F:462-479/Domain: transmembrane #status predicted <TM3>

F:512-533/Domain: transmembrane #status predicted <TM4>

F:549-572/Domain: transmembrane #status predicted <TM5>

F:643-668/Domain: transmembrane #status predicted <TM6>

F:710-727,809-825/Region: calmodulin binding #status predicted

F:722/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match

Best Local Similarity 4.3%; Score 262.5; DB 2; Length 1124;

Matches 181; Conservative 147; Mismatches 269; Indels 349; Gaps 43;

QY 295 DIVRWTKLQNTSHQHL-----LTVYDFEQQSESLDTVIL-----KALVK 336

Db 53 DHPNVRRLIQXLRHQHININCMIDLGRALTL-AIDNENLEWELVVMGVETKDALH 111

QY 337 ACKSHSQEQDYLDLKLAV-----ANDRVDIASSEIFNGDVKKSCDLEWWDALV 389

Db 112 AINAEFEVAVELLEHEELIYKEGEYSQKVDI-NTAMFAPDI-----TPMLAAH 162

QY 390 SKKPEFVRLFVNGA--DVADFLTYGRLOELYSVRKSLLPDLLQRKQEARLTLAIG 447

Db 163 KNNFELRLILDRGAALVPVPHDIRG-CCECVRLTDEBL-----RHSLSRYN 209

QY 448 TQOAREPP-----AGPAPSLHEVSRLVD--FLDADCRGFYODGPDRRRAEKGP 499

Db 210 IYRALCSPFLICLTSTNDPSSTAFOQLSWEELRNLLATLQCECKSEYMD---LRQCCQFAVD 265

QY 500 RRTGQKMLLDNOKSINPRDLFLMAVLQNRHEMATYFMAQOEGVAAALLACKIKENS 559

Db 266 -----LLDQRTSNE-----LAILLYVDPQSSY-----EPG----- 292

QY 560 HLETEAARATREAKYERLALDLFSECSNSEARAFALLVRNRCWSKTTCIHLATD 619

Db 293 -----DKMSL-----TRLVQALISK 307

QY 620 AKAFAHDVQAFLTRIMWDMVAAATPIR--LLGAFLCFALVYTNLTTFSEAPLRTG 676

Db 308 QKKFVAHNSIQQLSSITWD---GLPGRFRKSIYDKVICIAQV---AVLF----- 351

QY 677 LEDDLQDLSDLTEKSLYGL-----QSRVEELVEAPRAQGRPAVFLTRMRKFWGA 730

Db 352 -----FLYCLIYWCAPNCRGTQIM-----RK----- 372

QY 721 PTVPLGVNVMVFAFLPFLFTVLLV-----DERPPQSGSG 766

Db 373 PPMKFLIHASSYLFLFLF---LIVSQRADDDFVRIFGTRMKKELACQELRQSGTBSK 429

QY 767 PEVTLFVNFVLVLEIQGFTEDETHLVKKFTLYVDNNKNCMVAFLEFIVGTQM 826

Db 430 LELIVMVFVIGFVWEEOEIFAVGMS-----YLRNMNFIDFLNNSLY-VSWC-L 479

QY 827 LPSAFEARVTLAMD-----FMVFT-LRLIHIFAIHKOL 859

Db 480 RAFATIQQATEIARDPQAAVYIPREKMHDPDQLAEGFLAANVFSALKVHLEPSINHL 539

QY 860 GPKIIVERMMKDV--PFFLFELSYMLVAVGT-----TQALLPHDGLFW-- 904

Db 540 GPLQSLGRWIDIKYFFFTYTLVLFAPACGLQNLWYFAALEKSKCYLP-GBEADWS 598

QY 905 -----IRRV--LYRP-----YLOIFGQIPDEIDEAVNCSHTHLLDEBSCSYLAN 952

Db 599 HGDSCMKWRFRGNLFESSQSLFWASFGVVGDDFELSGIKS-----YTR 642

QY 953 WLVLITVPLTVTLVNLMLIAMFSYTFQVQGNATMFMFORYNLIVEYHERPA-LA 1011

Db 643 FWGLMFGSYIVNITVLLMLIAMMSYAMIDHSPTENKFARTKLMSTFEDSATLP 702

QY 1012 PFFILSHLSLTLRFRPKAEHKKREHLERDLPPLDQKVVTWETVQKENFLSKMKRR 1071

Db 703 PPFNVLPSPVKWVI-RIFRKS-----KIDRQSKKREQEQF 739

QY 1072 DSEGVLRKTAHRVDIFAKYGLGLEQ-----EKIKCLESQIN 1110

Db 740 SEYDINMR-----SLWRYVAAMHKKENNPVSEDDINEVSEIN 779

RESULT 8

F88391

Protein R06B10.4 [imported] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001

C:Accession: F88391

R:anonymus, The C. elegans Sequencing Consortium.

A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biology

A:Reference number: A75000; MID:99069613; PMID:9851916

A:Note: see websites genome.ucsf.edu/gsc/C.elegans/ and www.sanger.ac.uk/projects/C.e

A:Note: published extra appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and

A:Accession: F88391

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-899 <STO>

A:Cross-references: GB:chr_III; PIDN:AAB95033.1; PID:g2746879; GSPDB:GN00021; CESP:R06B1

A:Gene: R06B10.4

A:Map position: 3

Query Match

Best Local Similarity 3.9%; Score 239; DB 2; Length 899;

Matches 165; Conservative 125; Mismatches 313; Indels 252; Gaps 38;

QY 349 LDELKLAAMBRVDIAKEIFNGDVEMKSCD-----EEMVVALYSNKEPEFRLTV 401

Db 32 LREKQFLSCERGIDGVRKLKLAGISTTFNINCIDLGRNALILAIENENIEMLELLD 91

QY 402 NGADVADFLTYGRLOELYSVRKSLLPDLLQRKQEARLTLAIGTQOAREPPAPPA 460

Db 92 HNIETGDALIVAGEE---NVEAVETIYENLEKMDKPFSEROGVETHSATPTITPV 148

QY 461 FSLHVSRLKDFLODADCRGFYODGPDRRRAEKGPAPR-----TQCKWL 508

Db 149 LAAH-----KQNYE--CIKFLD-----KKGTVRPHRDVACSCPECVAAEEDSL 191

QY 509 DINQSENPRWDLFLMAVL-QNRHEMATYFMAQOEGVAAALLACKIKENSHLETEBA 567

Db 192 RLRSRINAYRALTSPSLICLSARDPIIYAFELSW-----LKRSLFIENEFRT 240


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Qy 568 ARATREANYERLALDPSSECSYNSSEAPAFALLVRNRCMSKTTG-----LHAT 616
Db 241 DYEELISQCKQCEVAMLDQVRGSEKLE--VVLNHTTNAMHDVTSANYGNPEKLARKLAI 298
Qy 617 EADAKAFPAHOGVOVAFIRIMWGDMAAGPILRLGAFLCFALVYTNLITPSEEPALRTG 676
Db 299 QLSQKRFPAHPNCQOOLLDIWY---EGVESVR-----CTNFIY-KLIY----- 338
Qy 677 LEDLDDLSLDEKSPLYGLQSRVEELVAPPAQDGRGPAVFLI--TRMKFPGAVPT 733
Db 339 -----ILGMLSPFLSL-----VYLLAPSSMGQFAKKPFI 369.
Qy 734 VFLGNVVMYFAFLFPTY-----VLVD-----FRPPGSGPSEVTLVFWFT 777
Db 370 KFLSHSGSYIFFLILLIMASQRMVYIDNLRDIDVRKRETRGP--PTIIECAIFLWVLG 427
Qy 778 LVLBEIRQ-----GFTDEDTHLVKGFPLYGDNMKCMVAIFLFIIVGTCML----- 827
Db 428 LIWEIKQIMBEGLYN-----YCRNLNMLDITNSLYLCTTALARVAVYQVE 475
Qy 828 PSAPFAAGR-----TVLAMPDPM-----VF-TLRIHIFAIHQQLGP-KII 864
Db 476 QEALRANSVHIAHLPKRDWDAMDPTLSECFPATANIPSSKLVIHITVSPHLGLPKIS 535
Qy 865 VVE-----RMKQDV--FFFLFPLSVMLVAVGTTQALHPHDGRLEWIFRRV- 909
Db 536 LGELLEKFWKKTKLKCRMYIDIVKFFMYVALVLFAPACGL-----NQLWVYAMR 585
Qy 910 -----LYRPY-----LQIFGQIPLDEIDEARVNGS-----THPILL 940
Db 586 QNECNLYQYQYKNEKSLSYKEHLKSCODKXKSCSISYHTAETLEFWALFGLVDLTHFRLK 645
Qy 941 EDSPSCPSLYANWLVILLVFLVNTVLMMLLAMPSTYPOVQGNATMFKQRYNL 1000
Db 646 ED-----HFLSEMTGKTIFGSCCSIIYVLMMLIAMMSNSQYISDQDIDEMKARSL 700
Qy 1001 IVEYHERPA-LAPFILL--SHLSLTLRVFKKAEKREHLERDLPPDLQKVVWET 1056
Db 701 FLEYDDTATLPPFPNIIVSPKSIYCYLHYLTKLCNCNCK-----LQQPSQKSM--R 751
Qy 1057 VQKFNFLSKMEKRR 1071
Db 752 VESKMLAIRORPRKO 766

```

RESULT 9

S44873
 ZC21.2 protein - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
 C:Accession: S44873
 R:Du, Z.; Waterston, R.
 submitted to the EMBL Data Library, May 1993
 A:Description: Sequence of the C. elegans cosmid ZC21.
 A:Reference number: S44649
 A:Accession: S44873
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-823 <DUZ>
 A:CDSa-references: EMBL:L16685; NID:q289729; PIDN:AAA28168.1; PID:q289732
 C:Genetics:
 A:Inserts: 47/2; 91/3; 144/1; 215/2; 344/3; 394/3; 440/3; 506/2; 566/3; 756/3
 C:Superfamily: TRPC3 protein
 C:Keywords: transmembrane protein

Query Match 3.8%; Score 234.5; DB 2; Length 823;

Best Local Similarity 20.7%; Pred. No. 1.3e-08;
 Matches 112; Conservative 92; Mismatches 195; Indels 143; Gaps 19;

Qy 549 LAACKILKEMSHLEFEAARAT---RAKYERLALDPSSECSYNSSEAPAFALLVRNR- 604
 Db 260 LSAFLSWDLQRLAFEEHEFKETIYQLSECKQYSDLLSQCRSSE--VIAIINKGNV 317

```

Qy 605 -----CWS---KTTCLHATEADAKAFFAHDGVOAFIRIMWGDMAAGTILRLGAF 655
Db 318 NDNIDWVASKLSTLSRLKLAIKYQKAFVSHPHQQLTSTLWY-----EGIYRQSGTWA 373
Qy 656 CFALVYTNLITPSEEPALRTGLEDDLSLDEKSPLYGL-----OSRVEELVAPRA 709
Db 374 NFFLYAFLLFWL-----PIFCIMYILMPKSRIGRLVRSP-- 407
Qy 710 QDGRPAVFLITMRKPGAVPTVFLGNVVMYFAFLFPTYVLLVD-----R 758
Db 408 -----FMKFFYVS-----FATFGLTLWATPEDRYRKGGRGNT 445
Qy 759 PPQPSGP--EVLTYFWVFTLVEEIRQGFTEDEDTHLVKGFPLYGDNMKCMVAIF 816
Db 446 ASDRGPATWESLVFTWVIGMLWSEIKQLM-----BEGFKRYRQNMNMDPLMIC 497
Qy 817 LFIIVGTCRMLPSAPE-----AGRTVLAMPVFTLRLLIHI 852
Db 498 LYLCTISIRL--SAVYIFTYREDPYRYTWTSEEBMLVABALFAVGAVFSPARITYL 555
Qy 853 FAHKQIGPKIIVERMMKQVFFFLFPLSVMLVAVGTTQALHPHDGRLEWIFRRVYR 912
Db 556 FQTPVYLGPIQISIGCMLVDKACFIPLIISFSIGLAQLWYYPDNTVCLPGATCK 615
Qy 913 PYLQIFGQIPLDEIDEARVNGSTHPLL-----EDSPSCPS-LYANMLVILLVTF 962
Db 616 HSNVPSFI-----ADSYLTILMSLFSITKEDEDTVDVENHKITQVCGGMFTMY 664
Qy 963 LVTNVLMLMLIMFSYTYPOVQGNATMFKQRYNL-IVEYHERPALAPF-ILLSHL 1020
Db 665 HCTSIIVLLMLIAMMSHSPQIINDHADLEWKFRHTKLMAMHPDEGSSLPPFPNIIVTPK 724
Qy 1021 SL 1022
Db 725 SL 726

```

RESULT 10

trp3 protein - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 07-May-1999
 C:Accession: J05807
 R:Preutz, K.D.; Noeller, J.K.; Krause, E.; Goebel, A.; Scholz, I.
 Biochem. Biophys. Res. Commun. 240, 167-172, 1997
 A:Title: Expression and Characterization of a trp1 homolog from rat.
 A:Reference number: J05807; MUID:98042538; PMID:9367904
 A:Accession: J05807
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-828 <PRB>
 A:Experimental source: brain
 C:Comment: This protein participates in store-operated Ca2+ entry into cells.
 C:Superfamily: TRPC3 protein

Query Match 3.1%; Score 186; DB 2; Length 828;

Best Local Similarity 19.7%; Pred. No. 4.4e-05;
 Matches 153; Conservative 122; Mismatches 291; Indels 210; Gaps 31;

Qy 381 EEWVADLVNKNPEFVRLFYDN-----GADVADFLTYGRLQELVRSVRKSL-LPDLQK 435
 Db 40 EERLDAAEYGNIFVVKMLBESSTLVNVCVDVGNALQ---LAVGNHLEVTLELLKK 96
 Qy 436 QEARKLTLAGI-----GTQAREPPAGRPAPSLHESRVVLKDFLQDRCRGFYDGRPGDR 490
 Db 97 ENLARIIDALLAISKGVYRIVEALISHPALAQOTLSPLR--LRD--DFFYUD----- 146
 Qy 491 RBAKGPAPKPT-----GQKW-----LLDINQSENMRDIFLVAVLQNRHEMAT-- 535
 Db 147 ---EDGTRFSDPTPIITLAAHCHRYEVVHLLLGKREPHDYVLCRCADCAEKORLWTF 203
 Qy 536 -----YFWANGQEGVANAALAAACKILKEMSHLEFEAARATREAKYERLA 580

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Db      204 HSRSRINAYKGSPEVLSLSSDDPVLTLHLSNELAKLANIEKEKRNDRKLSMCKQCFV 263
Qy      561 LDLFSECYSNSBARA-----FALLVRNRCSKTTCLHLATADAKAFPAHDGVAFLTR 635
Db      264 VGVLLDLCRDBSEVEAELILNDLDESVEERHGHKASLRVKLAIKYEYKFAVPCOQDLIT- 322
Qy      636 IWMGMMAAGTPIRLRLGAFLCFALVYTNLITFSEAPLRTGLEDQDDLSLTERKSPLYG 695
Db      323 IWMGMISGREIAIKCL-VLVVALLALPFLAIGWTAPC----- 359
Qy      636 LOSRVEELVEAPRAQDGRBRAVFLITRMKFGAPVTVFLGNVVM-----YEPFLFLPTY 751
Db      360 ---SRIGKILRSP-----FMKFAVASFIIFLGLVFNADREGITTLBN 401
Qy      752 VLLVD-----FRPPQSGSEPEVTLVFWFTVLVEIRGSEFTDEDTHLYKFFLYGDN 806
Db      402 ITVIDYPKOIFRVKTTQFTWTEMLIMVWVLGMMWSECKEIMLEGPREYIVOL----- 453
Qy      807 NKKCMVAIFLFIYGVTCMML----- 827
Db      454 KVVLLFLSTI-FLTAFTARFLAFLQATKAQOYVDHVSDELEVTLPREVQYFTYARDKM 511
Qy      828 ----PSAFAGRTVLAMDPMVFTLRILHIFALHKQIGPKIIVERMMKQVF-FFLFFLSV 882
Db      512 LPSDQITISEGLYALAV--VLSFSRIAYILPANESGPIQISGRVNDIIFKFWLFIWV 569
Qy      883 WL-----VAVGTTQALLHPHGRLEWIFRRVLYRPLYQIFGQIPLDEIDBARVNCST 935
Db      570 FLAFMIGMFLYSYLGAVDPAFTVEESFKTLFW---SIFG---LSEV-----T 614
Qy      936 HLLLEDSPSCPS---LYANMLVILLVTLPLVTLVLMNLIMAFSTFOVOGNATM 991
Db      615 SVALKYDHAFTIEIGVYLGIVNVTW-----VLLNMLIAINSSYQIEIDSDV 665
Qy      992 FMKFORYNLIVEYHERPALAPPEIL--LSHLSTLRRV-FKKEAEKREHLERLD 1043
Db      666 EKKFARSKMLSLFDDGKTLPPPLVPCRSPFYVIRIRYNPR---CRRRLRQKDI 718

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RESULT 11

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S68238
trp-1 proteain - human
C:Species: Homo sapiens (man)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 24-Sep-1999
C:Accession: S68238
R:Zhu, X.; Chu, P.B.; Peyton, M.; Birnbaumer, L.
FEBS Lett. 373, 193-198, 1995
A:Title: Molecular cloning of a widely expressed human homologue for the Drosophila trp
A:Reference number: S68238; MUID:96033971; PMID:7589464
A:Accession: S68238
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-793 <ZHU>
A:Cross-references: EMBL:U11110; NID:g1072042; PIDN:AAA93251.1; PID:g1072044
C:Superfamily: TRPC3 protein
C:Keywords: alternative splicing

```

```

Query Match      2.8%; Score 170.5; DB 2; Length 793;
Best Local Similarity 18.0%; Pred. No. 0.00055;
Matches 115; Conservative 106; Mismatches 216; Indels 203; Gaps 27;

Qy      555 LKEMSHLETE-----AEMARATREAKYERLALDLFSECYSNSBARAF----- 596
Db      244 LKELSLVEVEFRNDYBELAR-----QCKFAKDILAQARNSRELEVINHTSSDEPLDKR 298
Qy      597 ALLVRNRCSKTTCLHLATEADAKAFPAHDGVAFLTRIMGDMMA--GTPIRLLGAF 654
Db      299 GLLEER---MNLRLKLAIKYNOKEFVSQNSCOQFLNTVWFGQMSGYRRKPTCKKIMTV 354
Qy      655 LCFALVYTNLITFSEAPLRTGLELDQDDLSLTERKSPLYGQSRVEELVEAPRAQDGR 714
Db      355 LTVGIFW-----PVLSTCYLI-----APKSO----- 375

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Qy      715 PRAVFLTRMRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQSGSPG-----EV 769
Db      376 -----FGRITHTPRMKRIIHGASFTLLLNLSLV-YNEDKKTMTGMPALERIDY 425
Qy      770 TLFWVFTVLVEIRGQFTD-EDTHLYKFFTLVGDNMNKCDAVAFFLVGVTCMMLP 828
Db      426 LLIMTIOMISDIKRLWYEGLED-----FLEESRNQLSFVMSNLYLATFALKYVA 476
Qy      829 -----SAFEGRTVLAMDPMVFT-----RLHIFALHKQIGPKIIVERMM 870
Db      477 HNKFDPADRDMDAFHP--TLVABGLFAFANVLSTYLFVMTYTTSSILGPIQISMGML 534
Qy      871 KDV--FFFLFELSVLVAAGVTTQALLHPHGRLEWIFRRVLYRPLYQIF--GQIPLDEI 926
Db      535 QDFGKFLGMFLVLVLFSTIGLT-----QLYKGYTSKQK 569
Qy      927 D-----BARVNCSTHPLLLEDSPSCPELYANMLVI----- 956
Db      570 DCVGIFCEQSQNDTFHSFI---GTCFALF--WYIFSLAHVAIFVTRFSYGEILOSFYGA 623
Qy      957 LLLVFTLVTLVLMNLIMAFSTFOVOGNATMFMKFORYNLIVEY-HERPALAPPE- 1014
Db      624 VIVGTYNVVVVIVLTKLVAMLHKSFOLIANHEDEKEMFPAKRLWLSYFDKCTLPPPN 683
Qy      1015 -----ILLSHLSTLRRVFKKEAEKREHLE--RDLPPDLQKVVWETVQK----- 1059
Db      684 IIPSKTICWMLSSLSKIKCHTSKGVKQRNSLKEMNMLQKRD-----ENVYKMWCC 737
Qy      1060 --ENFLSKMEKRRRDBSEGVLRKTAHRVDFTAKYLGIRE 1097
Db      728 LVHRYLTSMRQMQSTDOATVENLNLRODLSKFRNEIRD 777

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RESULT 12

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138361
TRPC1 proteain - human
C:Species: Homo sapiens (man)
C:Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 04-Sep-1998
C:Accession: 138361
R:Wes, P.D.; Chevesich, J.; Jeromin, A.; Rosenberg, C.; Steceten, G.; Montell, C.
Proc. Natl. Acad. Sci. U.S.A. 92, 9652-9656, 1995
A:Title: TRPC1, a human homolog of a Drosophila store-operated channel.
A:Reference number: 138361; MUID:96003837; PMID:7568191
A:Accession: 138361
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-810 <RES>
A:Cross-references: EMBL:X89066; NID:g1019786; PID:g1019787
C:Superfamily: TRPC3 protein

```

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Query Match      2.8%; Score 170.5; DB 2; Length 810;
Best Local Similarity 18.0%; Pred. No. 0.00056;
Matches 115; Conservative 106; Mismatches 216; Indels 203; Gaps 27;

Qy      555 LKEMSHLETE-----AEMARATREAKYERLALDLFSECYSNSBARAF----- 596
Db      261 LKELSLVEVEFRNDYBELAR-----QCKFAKDILAQARNSRELEVINHTSSDEPLDKR 315
Qy      597 ALLVRNRCSKTTCLHLATEADAKAFPAHDGVAFLTRIMGDMMA--GTPIRLLGAF 654
Db      316 GLLEER---MNLRLKLAIKYNOKEFVSQNSCOQFLNTVWFGQMSGYRRKPTCKKIMTV 371
Qy      655 LCFALVYTNLITFSEAPLRTGLELDQDDLSLTERKSPLYGQSRVEELVEAPRAQDGR 714
Db      372 LTVGIFW-----PVLSTCYLI-----APKSO----- 392
Qy      715 PRAVFLTRMRKFWGAPVTVFLGNVVMYFAFLFTYVLLVDFRPPQSGSPG-----EV 769
Db      393 -----FGRITHTPRMKRIIHGASFTLLLNLSLV-YNEDKKTMTGMPALERIDY 442
Qy      770 TLFWVFTVLVEIRGQFTD-EDTHLYKFFTLVYGDNMNKCDAVAFFLVGVTCMMLP 828
Db      770 TLFWVFTVLVEIRGQFTD-EDTHLYKFFTLVYGDNMNKCDAVAFFLVGVTCMMLP 828

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Db 443 LILIMIGMINDIKRMIEGLED-----FLEESRNOISFVANSIYATPALKYVA 493
 Qy 839 -----SAFEAGRTVLANDFMVT-----LRLIHFAIHKQGPXIIVERMM 870
 Db 494 HNKHFHADRKMDAFHP--TLVAEGLFAFANVLSTLRFPMYTTSSILGPIQISMGOVL 551
 Qy 871 KDV--FFPLFELSVMLVAVGTTQALLPHDGRLEKIFRRVLYRPLYQIF--GQIPLDEI 926
 Db 552 QDFKFLGMFLVLVLPFTIGLT-----QLYDKGYSKEQK 586
 Qy 927 D-----EARNVCSGTHPILLEDSPSCPSLYANMLVI----- 956
 Db 587 DVGIFCEQSSNDTPHSFT-----GTCFALF--WYIFSLAHVAIPVTRSYGELQSPVGA 640
 Qy 957 LILVTFELVTLVNLMLLIMESYTFQVQGNATWFKFORNLIYEV--HERPALAPP- 1014
 Db 641 VIVGYNNVVVIVLTKLVAMLHKSFQLIANHEDKEMKAKAKMLSYDDKCTLPPEPN 700
 Qy 1015 -----ILSHSLTLRRVFKKEAEHKEHLE--RDLPLDQKVWTETVOK--- 1059
 Db 701 IIPSEKTCIYMTSSLSKWCISHTSKGKVRQMSLKEMRNLKQKRD-----ENYQKVMCC 754
 Qy 1060 --ENFLSKMEKRRRDEGEVLAKTARVDFIAKYGLRE 1097
 Db 755 LVHRYLTSMRQKQSTQATVENLNELRQDLSKFNEIRD 794

RESULT 13

734472.
 hypothetical protein W03B1.2 - Caenorhabditis elegans
 CSpecies: Caenorhabditis elegans
 CDate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 CAccession: T34472
 RMiller, N.; Bradshaw, H.; Wu, X.; Gattung, S.
 submitted to the EMBL Data Library, June 1998
 ADescription: The sequence of C. elegans cosmid W03B1.
 AReference number: Z21532
 AAccession: T34472
 AStatus: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-823 <Mtu>
 A.Cross-references: EMBL:U58753; PINN:AAC24437.1; GSPDB:GN00022; CESP:W03B1.2
 A.Experimental source: strain Bristol NZ; clone W03B1
 C.Genetics:
 A.Gene: CESP:W03B1.2
 A.Map position: 4
 A.Introns: 70/3; 102/1; 137/2; 187/2; 265/3; 293/3; 357/3; 489/3; 516/1; 604/2; 628/2

Query Match 2.7%; Score 166; DB 2; Length 823;

Best Local Similarity 22.4%; Pred. No. 0.0012;

Matches 99; Conservative 64; Mismatches 172; Indels 106; Gaps 19;
 Qy 771 LYFWFTLV-----LEIRQ--GPTDEDTHLVKKFTLYGDNKKCDMAIFLFIYGV 822
 Db 406 LAFWRIVLVPLLTLEAARLLIFAVIEKKSSDKNF-----WSGA-----WVLPI 452
 Qy 823 TCRMLPSAFBAGRTYLANDFMVTFLRIIIFAIHKQGPXIIVERMMKV--FFPLFPLS 881
 Db 453 TLELLYKALFAIAT-----VSTARFHSIT--OSLGFTHLFKKMKTKVMFLICT 502
 Qy 882 VWLVAVGTTQALLPHDGRLE-----EWIFRRVLYRPLYQIFGQIPLDEIDARV---N 932
 Db 503 FWFVL-----AVIVSISRLLTATNSNPLYVTVOGKEIGEVQ---DEDRIQILN 552
 Qy 933 CSTHLLLED-----SPSCPSLYANMLVILVTLVTLVNLMLLIMESYTFQV 985
 Db 553 CSEYKTKWEPFDMVEAESC--LFRSTIMPRVFTYIFVIGILLVNLTLAQITREYNE 610
 Qy 986 QGNATWFKFORNLIYEVHERPALAPPIL----- 1017
 Db 611 SKNSAYVYGYLKYEDQTKESLALPPPSLTVVULRFVYSCFFKYIYITTWLTSGCCK 670
 Qy 1018 ---SHLSLTLRRVFKKEAEHKEHLELDPLDQKVWTETVOKENFLSKME-----K 1068

Db 671 CSTAISLSLWNRNIVRIYEGVPGCAVROTDNEIDTKVAEFLRKPDPNALETKDLVNNYD 730
 Qy 1069 RRPDEGEVLAKTARV--DPIAKYLGRLREDEKIKIESQINCSYVSSVADVLAAQG 1127
 Db 731 KQVDD--EALKKLGKEIKKFLAKEIG--EERERQSNLENHPRSGSVLDPKKGRLS--- 784
 Qy 1128 GPRSSQHCESGSQLVAADHRC 1148
 Db 785 --RTFAPVPGSSAVSLDQEG 803

RESULT 14

528916
 dystrophin - mouse
 N.Alternate names: duchenne muscular dystrophy protein
 CSpecies: Mus musculus (house mouse)
 CDate: 22-Nov-1993 #sequence_revision 03-Nov-1995 #text_change 16-Jul-1999
 CAccession: S28916; B27162; S10922; C43837; B40134
 R.Bies, R.D.; Phelps, S.F.; Cortez, M.D.; Roberts, R.; Caskey, C.T.; Chamberlain, J.S.
 Nucleic Acids Res. 20, 1725-1731, 1992
 A.Title: Human and murine dystrophin mRNA transcripts are differentially expressed during
 A.Reference number: S28916; MUID:92253376; PMID:1579466
 AAccession: S28916
 AStatus: preliminary; nucleic acid sequence not shown; translation not shown
 A.Molecule type: mRNA
 A.Residues: 1-3678 <BIE>
 A.Cross-references: EMBL:M68859
 A.Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1991
 R.Koenig, M.; Hoffman, E.P.; Bertelson, C.J.; Monaco, A.P.; Feener, C.; Kunkel, L.M.
 Cell 50, 509-517, 1987
 A.Title: Complete cloning of the Duchenne muscular dystrophy (DMD) cDNA and preliminary
 A.Reference number: A90897; MUID:87273512; PMID:360877
 AAccession: B27162
 A.Status: not compared with conceptual translation
 A.Molecule type: mRNA
 A.Residues: 1-201 <KOE>
 R.Nudel, U.; Zuk, D.; Einat, P.; Zeelon, E.; Levy, Z.; Neuman, S.; Yaffe, D.
 Nature 337, 76-78, 1989
 A.Title: Duchenne muscular dystrophy gene product is not identical in muscle and brain.
 A.Reference number: S06461; MUID:85082658; PMID:2909892
 AAccession: S10922
 A.Status: translation not shown
 A.Molecule type: mRNA
 A.Residues: 1-106 <NUD>
 A.Cross-references: EMBL:X14183
 R.Rapaport, D.; Lederlein, D.; den Dunnen, J.T.; Grootscholten, P.M.; Van Ommen, G.J.; F
 Differentiation 49, 187-193, 1992
 A.Title: Characterization and cell type distribution of a novel, major transcript of the
 A.Reference number: A43837; MUID:92316332; PMID:1377655
 AAccession: C43837
 A.Status: preliminary
 A.Molecule type: mRNA
 A.Residues: 1-MREHLKG, 3069-3181 <RAP>
 A.Note: sequence extracted from NCBI backbone
 R.Hoffman, E.P.; Monaco, A.P.; Feener, C.C.; Kunkel, L.M.
 Science 238, 347-350, 1987
 A.Title: Conservation of the Duchenne muscular dystrophy gene in mice and humans.
 A.Reference number: A40134; MUID:88018015; PMID:3659917
 AAccession: B40134
 A.Status: preliminary
 A.Molecule type: mRNA
 A.Residues: 300-676 'F', 678-1390 <HOF>
 A.Cross-references: GB:M18025
 C.Genetics:
 A.Introns: 11/1
 A.Note: The list of introns may be incomplete
 CSuperfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystropi
 CKeywords: actin binding; alternative splicing
 F.14/233/Domain: alpha-actinin actin-binding domain homology <ACT>
 F.340-449/Domain: spectrin/dystrophin repeat domain homology <SP1>
 F.450-558/Domain: spectrin/dystrophin repeat homology <SP2>
 F.2797-2924/Domain: spectrin/dystrophin repeat homology <SP3>

F:3048-3085/Domain: WW repeat homology <WW1>

```

Query Match      2.7%; Score 164.5; DB 2; Length 3678;
Best Local Similarity 19.9%; Pred. No. 0.015;
Matches 158; Conservative 99; Mismatches 266; Indels 269; Gaps 36;

QY 60 WHLPANLVSVSGEPPPMKSMWLRDV-----LRKGLVKAASGTGAMITLSALRVG 111
DB 2228 WLEADNVAITPLGDQ--QLKEQLQVTLAELEPLRGILKQINLETGAVLVSA----- 2281
QY 112 LARHVGQAVRDSLASTSTKRVVAVGASLGRVLRRLLEAQRDPVHYBEDDGSOG 171
DB 2282 -----PIRPEODLKKLTK-----QTNLQWIKVSRALEPKQGLEVHLKD----- 2322
QY 172 PLCSLDSNLSHFL-VEPGPGKGDGLTELRLRLKEHSEORAGVGTGSIEI----- 223
DB 2323 -FRQLEBQDHLHLWSP-----IRNQLLEYNOPSQAGPPDIKEIETVYHGKQA 2370
QY 224 PVLCLLVNGD-----PNTLERISRAVE-----QAAFWLILVGS 256
DB 2371 DVERLLSKQOHLYKEKPSR-QPVKRLLEDLRSEWAVNHLRLKQDPRAFGISTGA 2429
QY 257 GGIADVLALVNPVHLLVPRVAKQPKPKP-----HFSMEDIVRWTKLON 305
DB 2430 S--ASQTVTLVTSVVTKEVTSKL--EMPSLLLEVPALADFNRAWTELTDMLSLDR 2484
QY 306 IISHQHL-----TYDDEQSGSELDVILKALVYKAKSHSQEPQDVL 349
DB 2485 VKSKQVWVGDLIEDINEMITIKOKATLODLEOR-RPQLEELITVAONLKNKTSNQEARITII 2543
QY 350 DEL--KLAVAMPDV-----IAKSEIFNGDVEMWSC--DLEEVW----- 384
DB 2544 TRIRIEIQOMQEVGQOLNRQQLNEMLKDSQWLEAKEEAOVIGYRGLKDSWKEGP 2603
QY 385 --VDALVSKPEPFLVD---NGADVADFLTYGRLOELYSVSRKSLFDLLORQOE 437
DB 2604 HTVDALQKKTETKQAKDLRQKQISVDVANDLALTLRDYSADPTRK---VAMITE 2657
QY 438 EARLTLAGGTQARPPAPRPAFSLHEVSRVLKDF-----LQDA 477
DB 2658 NINTSGNTHKRVSEDEA-----LEETHRLQOFPDLLEKFLSMTTAEATTANVLQDA 2711
QY 478 CR--GFYQDGRPRDERRAE---KGPAPKPT-----GQKMLDLNOKSENFWMDL 521
DB 2712 SKREKLEDSR-GVRILMKPMQDLOGEIEHTHDIYNNLDENGKILRSLESGSEAR---- 2766
QY 522 FIMAVLQNRHEMATYVWAMGQSVAAALAACTLKEMSHLETAAPARTREAKTERLAL 581
DB 2767 ---LQRLRDNNNFKWSELOK-----KSLNIRSHLEASSD-----QMKRLHL 2805
QY 582 DLFSECVSSEARAFALVRRNCWSKTCMLATEADAKAPFAHDGQVAFRLRWGM 641
DB 2806 SLOE-----LLV-----WLQKDELISRQAPIGDPVAVOKNDIHRARKRL 2848
QY 642 AAGTPIRLLAGAFCLFALVYTNLITFSEBAPLRTGLEDIQDLSLDTKSPSLYGQSRVE 701
DB 2849 KTKEPVI-----WSTLETYRIFLITEQ-PLEGLEKLYQ 2879
QY 702 ELVEAP--RAQ 710
DB 2880 EPRELPPERRAQ 2891

```

RESULT 15

S61648
probable membrane protein YOR088w - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: hypothetical protein O3151; hypothetical protein YOR3151w
C:Species: *Saccharomyces cerevisiae*
C:Date: 09-Mar-1996 #sequence_revision 12-Apr-1996 #text_change 19-Apr-2002
C:Accession: S61648; S66973
R:Benes, V.; Andrade, M.A.; Rechmann, S.; Teodoru, C.; Banreivi, A.; Sander, C.; Valencia
submitted to the EMBL Data Library, December 1995
A:Description: Nucleotide sequence and analysis of a 130 kb fragment of yeast chromosome

```

A:Reference number: S61643
A:Accession: S61648
A:Molecule type: DNA
A:Residues: 1-482 <BEN>
A:Cross-References: EMBL:X94335; NID:g1262139; PID:g1164934
A:Vose, H.; Benes, V.; Rechmann, S.; Teodoru, C.; Schwager, C.; Paces, V.; Ansoerge, W.
submitted to the Protein Sequence Database, July 1996
A:Reference number: S66965
A:Accession: S66973
A:Molecule type: DNA
A:Residues: 1-482 <VOS>
A:Cross-References: EMBL:Z74995; NID:g1420253; PID:g1420255; MIPS:YOR088w
A:Experimental source: strain S288C
A:Genetics:
A:Cross-References: SGD:S0005614
A:Map position: 15R
C:Superfamily: Saccharomyces cerevisiae probable membrane protein YOR088w
C:Keywords: transmembrane protein
F:46-62/Domain: transmembrane #status predicted <TM1>
F:159-175/Domain: transmembrane #status predicted <TM2>
F:184-200/Domain: transmembrane #status predicted <TM3>
F:251-267/Domain: transmembrane #status predicted <TM4>
F:328-344/Domain: transmembrane #status predicted <TM5>

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Query Match      2.5%; Score 153.5; DB 2; Length 482;
Best Local Similarity 20.1%; Pred. No. 0.0044;
Matches 95; Conservative 79; Mismatches 151; Indels 147; Gaps 19;

QY 702 ELVEAPRAQGR-----GPAVFLTRMRKFGAVTVPLGNVWVFAPFLFTYVL 753
DB 4 ERMDSPKMLGSHNFYQGRFTGSVIDLSFQPKKRGACIPKLFADLL--ILFLGLYTL 60
QY 754 LVDFRPPQSGSPGPEVTLTYFWFT--LVLEIRQGF-----DEDTHLVKKFT 800
DB 61 VVNGDSERVQSFLLSEIFVYFNTGFIIDELTKLYIGYALHSFNNLFNDITTYLITFA 120
QY 801 L-----YVGNMNMKCDVVALFLFVGTGCMLEBSA--FEAGRTVLAAMDWFV 845
DB 121 MGFRAVSATPLNAKYSSEDMK-----ISYVLSCAAPFVMSRLILYLESQRF 168
QY 846 TURLHIAHAKQGLPKIIVVERMKD--VFPELFELSVMLVAVYVTTQAL-LNHHDRL 902
DB 169 -----IGIMLVILKHMKEISIVFFLLF-----LIMGTGFGGLDSADKR 211
QY 903 EMIFRVLVRYPLQIFQGIPLDEIDEARVNSTHLLLEDSPCSLYANMLVILLYTF 962
DB 212 D-ITGPILGNLITTYVLGSGPVEE-----PAPRYAAILYYGY 249
QY 963 LLVTNVLMLNLIAFSTYFOVQGN-----ATWFMKFORV-----NLI-- 1001
DB 250 YFIVSVILLNLIALYSTAVQGVINDADDEVWALMSQKTLRYIRAPDEDVYVSPNLIEV 309
QY 1002 -----VEYHERPALAPPILLSHLSTLRLRVFKKEAEHKEHLERDLPD 1045
DB 310 FWTPIFRILPPKRAKLSYTWITVYSPFLILISYK-----REARIRKRMKRLND 363
QY 1046 PLDQKVVVMEYQ-----KENFLSKMEKR-RDSEGEVLKRTARVD 1086
DB 364 DANEDYTPWDLTDGYLDGDDGLFSDRNSGKRAIOLKNSRSLSKLORTAQED 415

```

Search completed: September 10, 2003, 09:41:55
Job time : 34 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2003, 09:27:29 ; Search time 17 Seconds

(without alignments)
3222.712 Million cell updates/sec

Title: US-09-834-792C-4

Perfect score: 6091
Sequence: 1 MDVVGPPRPGSGDAEDRRE.....HRGGIDGWEQPGAGQPSDT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2041	33.5	1503	TRL2_HUMAN	Q94759 homo sapien
2	655	10.8	1017	TRL3_HUMAN	Q9hcf6 homo sapien
3	318	5.2	1275	TRP_DROME	P19334 dirosophila
4	290	4.8	1418	CEIL_CAEEL	P34641 caenorhabdi
5	262.5	4.3	1124	TRPL_DROME	P48994 dirosophila
6	258.5	4.2	1172	TRP2_MOUSE	Q9c744 mus musculu
7	244	4.0	885	TRP2_RAT	Q9t883 rattus norv
8	239	3.9	1027	TRPL_CAEEL	P34586 caenorhabdi
9	231	3.8	974	TRP5_HUMAN	Q9u162 homo sapien
10	231	3.8	974	TRP5_RABIT	Q62852 cryctolaqus
11	231	3.8	975	TRP5_MOUSE	Q9qkx29 mus musculu
12	221	3.6	981	TRP4_BOVIN	P79100 bos taurus
13	219.5	3.6	977	TRP4_HUMAN	Q9ubn4 homo sapien
14	216	3.5	974	TRP4_MOUSE	Q9quq5 mus musculu
15	216	3.5	977	TRP4_RAT	Q95119 rattus norv
16	194	3.2	931	TRP6_HUMAN	Q9y210 homo sapien
17	193	3.2	862	TRP7_HUMAN	Q9hcx4 homo sapien
18	190.5	3.1	836	TRP3_MOUSE	Q9qcx1 mus musculu
19	187	3.1	862	TRP7_MOUSE	Q9qwc5 mus musculu
20	183	3.0	930	TRP6_MOUSE	Q61143 mus musculu
21	180.5	3.0	848	TRP3_HUMAN	Q13507 homo sapien
22	179.5	2.9	736	TRP3_RAT	Q9jmi9 rattus norv
23	178.5	2.9	759	TRP1_RABIT	Q9tun9 cryctolaqus
24	171	2.8	793	TRP1_BOVIN	Q18784 bos taurus
25	170.5	2.8	759	TRP1_RAT	Q9q401 rattus norv
26	170.5	2.8	793	TRP1_HUMAN	P48959 homo sapien
27	170.5	2.8	809	TRP1_MOUSE	Q61056 mus musculu
28	164.5	2.7	3678	DMD_MOUSE	P11531 mus musculu
29	152	2.5	432	TRP2_BOVIN	Q62826 bos taurus
30	150	2.5	968	PKD2_HUMAN	Q13563 homo sapien
31	148.5	2.4	966	PKD2_MOUSE	Q35245 mus musculu
32	140	2.3	3680	DMD_CANFA	Q97592 canis fam11
33	136	2.2	5596	DMD_HUMAN	Q9nu22 homo sapien

34	132	2.2	830	1	VPP3_HUMAN	Q13488 h vacuolar
35	130.5	2.1	2390	1	SCCP_HUMAN	Q15020 homo sapien
36	129.5	2.1	1261	1	APAF_BRARE	Q919h8 brachydantio
37	128.5	2.1	3685	1	DMD_HUMAN	P11532 homo sapien
38	128	2.1	621	1	P212_MOUSE	Q911g4 mus musculu
39	126.5	2.1	2388	1	SCCP_RAT	Q9qwm8 rattus norv
40	124.5	2.0	1835	1	CCAI_RAT	Q920Y8 rattus norv
41	124.5	2.0	5065	1	EBPL_HUMAN	P58107 homo sapien
42	123.5	2.0	2223	1	CCAI_HUMAN	Q960x4 homo sapien
43	123	2.0	1060	1	AZII_MOUSE	Q62036 mus musculu
44	120	2.0	2019	1	CIN5_RAT	P15389 rattus norv
45	119	2.0	1087	1	XPO7_HUMAN	Q9uia9 homo sapien

ALIGNMENTS

RESULT 1
ID TRL2_HUMAN STANDARD; PRT; 1503 AA.
AC Q94759; Q96XN6;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Long transient receptor potential channel 2 (TRPC2) (Transient
DE receptor potential channel 7) (TRPC7).
GN TRPM2 OR TRPC2 OR TRPC7 OR KMP3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Brain;
RX MEDLINE=99026133; PubMed=9806837;
RA Nagamine K., Kudoh J., Minoshima S., Kawasaki K., Ito F.,
RA Shimizu N.;
RT "Molecular cloning of a novel putative Ca2+ channel protein (TRPC7)
RT highly expressed in brain.";
RL Genomics 54:124-131(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX Wehage E., Eisfeld J., Heiner I., Juenling E., Zilt C.,
RA Lueckhoff A.;
RT "Splice variants of TRPC2 differentially activated by ADP-ribose an
RT hydrogen peroxide.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20289799; PubMed=10830953;
RA Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,
RA Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,
RA Soeda E., Ohki M., Takegi T., Sakaki Y., Taudien S., Blechschmidt K.,
RA Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
RA Rosenthal A., Rump A., Schillhaber M., Schudy A., Zimmermann W.,
RA Reischwald K., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
RA Shintani A., Saeki T., Nagamine K., Mitsuyma S., Antonarakis S.E.,
RA Minoshima S., Shimizu N., Nordliek G., Hornischer K., Brandt P.,
RA Scharte M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecher H.,
RA Ramser J., Beck A., Klages S., Hennig S., Rieseemann L., Dagand E.,
RA Wehmer J., Borzym K., Gardiner K., Nizetic D., Francis F.,
RA Lehnach H., Reinhardt R., Yaspo M.-L.;
RT "The DNA sequence of human chromosome 21.";
RL Nature 405:311-319(2000).
CC -1- FUNCTION: MAY BE A CALCIUM CHANNEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing: Named isoforms=2;
CC Comment=Additional isoforms seem to exist;
CC Name=1;
CC IsoId=Q94759-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q94759-2; Sequence=VSP_006574, VSP_006575;
CC

CC	-!	TISSE SPECIFICITY: Highly expressed in brain.
CC	-!	SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. LTRPC SUBFAMILY.
CC	-!	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/isb-sib.ch).
DR	EMBL:	AB001535; BAA34700.1; -
DR	EMBL:	AJ417076; CAD01139.1; -
DR	EMBL:	AP001754; BAA95563.1; -
DR	GeneW:	HGNC:12339; TRPM2.
DR	MIM:	603749; -
DR	GO:	GO:0005887; C:integral to plasma membrane; TAS.
DR	GO:	GO:0005262; F:calcium channel activity; TAS.
DR	GO:	GO:0006816; F:calcium ion transport; TAS.
DR	InterPro:	IPR002111; Cat channel_Trlp.
DR	InterPro:	IPR005821; Ion trans_
DR	InterPro:	IPR002153; Trans_receptor.
DR	Pfam:	PF00520; ion trans_I.
DR	Pfam:	PF00293; NUDIX_1.
DR	PRINTS:	PR01097; TRANSMRECEPTR.
KW	Ionic channel;	Transmembrane; Ion transport; Calcium channel;
KW	Alternative splicing:	
FT	DOMAIN	1 752 CYTOPLASMIC (POTENTIAL) .
FT	TRANSMMEM	753 773 POTENTIAL.
FT	DOMAIN	774 795 EXTRACELLULAR (POTENTIAL) .
FT	TRANSMMEM	796 816 POTENTIAL.
FT	DOMAIN	817 820 CYTOPLASMIC (POTENTIAL) .
FT	TRANSMMEM	821 841 POTENTIAL.
FT	DOMAIN	842 896 EXTRACELLULAR (POTENTIAL) .
FT	TRANSMMEM	897 917 POTENTIAL.
FT	DOMAIN	918 936 CYTOPLASMIC (POTENTIAL) .
FT	TRANSMMEM	937 957 POTENTIAL.
FT	DOMAIN	958 1025 EXTRACELLULAR (POTENTIAL) .
FT	TRANSMMEM	1026 1046 POTENTIAL.
FT	DOMAIN	1047 1503 CYTOPLASMIC (POTENTIAL) .
FT	VANSPPLIC	538 557 Missing (in isoform 2) .
FT	VANSPPLIC	1291 1325 /FTID=VSP_006574.
FT	DPLEBLSTIQNVNVDGLDRNSFHGPYVQAGLP	-> E (in isoform 2) .
FT	CONFLICT	1088 1088 /FTID=VSP_006575.
FT	CONFLICT	1189 1189 S -> N (IN REF. 2) .
FT	SEQUENCE	1503 AA; 171225 MW; AD329AE79F1A71B5 CRC64;
Query Match	33.5%;	Score 2041; DB 1; Length 1503;
Best Local Similarity	38.8%;	Pred. No. 4,4e-129;
Matches	459;	Conservative 200; Mismatches 399; Indels 124; Gaps 23
Oy	26	GEVNFGSGGGKKRKGVVRPSGVASVLEDDLIAENHLRPAPNLVSLVGBEOPFAMKMYLR 85
Db	128	GDIYVTGTSLOAKYKKXRVSDPTSSVIYHLMQHGLVDPNNLLISVTGAKNFNMKPRLK 187
Oy	86	DVLKRGVLKAQNSTAMITLSLRGLARHGQAQRDHSIASTSKRVAVNVGNASLRRV 145
Db	188	SIFRGLVKVAQTITAMITLTGSHTGVNKQGEAYRDSLSYSYEGELITIGAVTWGTV 247
Oy	146	LHRRIIEAEOEDFPVHYPEDDGSGOCPCLSDSNLSHFIVBERPGPKGDGLTELRILE 205
Db	248	HRRESLIHPITGSFFPAEYLIDDEG-QGNLTCLDSNNSHFLVDDGHGQGYVEIRLTRLE 306
Oy	206	KHISQRAQYGSTGSIETPVLCCLLVNDPNTLERISRAVEOAAPWLIVGSGGIADVIAA 265
Db	307	KFISQTERGERGV-AIKIPIVCVVLEVGGPGLTIHDNAATTNGTPCVAVVVGSGSRVADVIAQ 365
Oy	266	LVNQD--HLVNPKVAKEQ---FKKEFRKPHSMEDIYATWKLLQNITSHOHLLTYUDEQ 320
Db	366	VANLPSVDITTLISLOOKLSVFPEQEFET--FTESRIVMETKIDIVRRRODLLVFRGK 423

QY	321	EGSEELDTVLIALVKACKSHSQEPOVDL-ELKLVAMDSVDLAKSIIPNGDVBMKSD	379
Db	424	DGQDQDVDAIIQALLKASRSQDFHGEHWMDDQKLKLVAMNRDLARSEIPMDEWMQKSD	483
QY	380	LEEVNVDLAVNKEEFVRLFVNDGNADVDFLTYGRLQELYRSVSRKSLFFDLQKOEBA	439
Db	484	LHPMTAALINKKEFVRLFLENGVQLKEFTYMDTLVLYENLDPSCLFHSKLQK----	538
QY	440	RLTLAIGTQOAREBPAPR--PAPSLHEVSRYLKDFLODACRGFYQDGRPGDRR----	492
Db	539	-----VLVEDPERPACAPAPRLQMHNVAAQVLEELLQDFQPLPYRPRHRNDRLFLLPV	592
QY	493	-----AEKRAPRPTGQKMLDLDNQSENPBRLFLFMAVLQNHMATYMWAMQO	542
Db	593	PHYKLNVQGVSLRSLYKSSGHVTF-----TMDIRDLIWAIQNRRLNGITWASQO	646
QY	543	EGVAALAALACIKLEMSHLETEAAR--ATREAKYERLADLPSECYSSNBARAFLL	599
Db	647	DCIAAALACSIILKELISEEDTQSEEMLLAE-EYEHRAIGVTECYRDEBRAQKLL	705
QY	600	VRRNRCSKTTCLHLATEADAKAPFADGVQAFLTRIMGDMAGTPTLLRLGALCPAL	659
Db	706	TRVSEANGKTTCLDLAEAKMKKEVSHOGIQAFLTKVMQGLSDNGLMRYLLCMLAEP	765
QY	660	VYTNLLPSEEARPLRTGLEDLDODLSDTBSPLYGQSRVETLEAPRAQODRGPRAVF	719
Db	766	LITGLISPREK-----LQD-----VGTPAA-----	786
QY	720	LITWRKRWGAPVTVFELGNVVMYFAFLFTYVLLVDRPRPQSGSEVTLYFWVFTLV	779
Db	787	---BARAFPTAPVVVFNHLNLSYFAFLCLFAYVLMVDQPV---PSWCECAIYMLFSLV	840
QY	780	LEETROGFTDEBDHLVKKFTLVYGDMMKCKDMAIPLFIYGVCMRLPSAPFEGRTVLA	839
Db	841	CEMRQLEFYDDECGLMKKALYFSDFMNKLQDVGAILLFVAGLTCRLIPATLYPERVILS	900
QY	840	MDFWFTLRLLHIFAIHQLQPKLIIVERRMKQDVEFFLFFSLVAVAGVTTQALLHPHD	899
Db	901	LDLFLFCRLMHITISIKTLQPKLIIVGRMKQDVFFFLAVVAVVSGVAKQALLINE	960
QY	900	GRLEWIFRRVLVYRPLQIFQGIPL-LDEIDARVNC--THPLLEDSPECS-----	948
Db	961	RRVWMLFPGAYVHLYLTFQGIPEGIDGVNPNPCHSGNGNDPY---KPKCPESDQO	1010
QY	949	--LVANMLVLLLTETLLVTNVLNMLNLIAESYTFQVQGNATYMFKFORYNLVEYHE	1000
Db	1017	RPAPREMTVLLLCVLYFTLLNLLNLIAFNNTIQQVOQHTDQIMKFOHNDLEETHG	1070
QY	1007	RPALAPPELLSHSLTLRVFKKEAEKREHLENDLPDLQKVVTWETQKENFLSKM	1066
Db	1077	RPAPREPELLSHQLFIKRVLVLTAPRAHNLQNLKLEKNEBALMSMEIYIKENYLNQR	1133
QY	1067	EKKRRDSEGEVLRKTAHRVFIATYLL-----GGLREQEKIKLESQINCYGVVSS	1113
Db	1137	QFOQKORPEQKIEBISNVKDMVLLDLDPKRSQSM--EQRSLSEVOVAQTARALHW	1193
QY	1119	VADVLAQGGGRSSQHCQSGSQLVAAD--HRGIDGWEQSG	1157
Db	1194	IVRTLPRASGSSEADVPTLMSQKAABEPDAEPGGKKTBEFG	1235

RESULT 2

TRL3_HUMAN ID TRL3_HUMAN STANDARD; PRT: 1017 AA.

AC Q9HCF6;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Long transient receptor potential channel 3 (Ltrpc3) (Fragment).

GN TRPM3 OR LTRPC3 OR KIAA1616.

NC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20450683; PubMed=10997877;
 RY Nagase T., Kikuno R., Nakayama M., Hirosewa M., Ohara O.,
 RT "Prediction of the coding sequences of unidentified human genes.
 RV XVII. The complete sequences of 100 new cDNA clones from brain which
 RW code for large proteins in vitro."
 RL DNA Res. 7:273-281(2000).
 CC -1- FUNCTION: MAY BE A CALCIUM CHANNEL.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. TRPC
 CC SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC -----
 DR EMBL; AB046836; BABJ3442.1; -.
 DR Genew; HGNC:1792; TRPM7.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR Pfam; PF00520; Ion_trans_1.
 KW Ionic channel; Transmembrane; Ion transport; Calcium channel.
 FT NON_TER 1
 FT TRANSMEM 80 100 POTENTIAL.
 FT TRANSMEM 183 203 POTENTIAL.
 FT TRANSMEM 250 270 POTENTIAL.
 FT TRANSMEM 314 334 POTENTIAL.
 FT TRANSMEM 402 422 POTENTIAL.
 FT TRANSMEM 453 473 POTENTIAL.
 SQ SEQUENCE 1017 AA; 116681 MW; B088354F100A972C CRC64;
 Query Match 10.8%; Score 655; DB 1; Length 1017;
 Best Local Similarity 28.0%; Pred. No. 4,66-36;
 Matches 171; Conservative 132; Mismatches 250; Indels 58; Gaps 14;
 OY 576 YERLALDLFSECYSSEARAFALVRRNRCSKTCCLHLEADAKAFADGVQAFTR 635
 DB 10 FGQALVELLDQSYKQDEQLAKMLTYELKMSNATCLOLAVAKRDIAHTCSMLTLD 69
 OY 636 IWWG--DMAAGTPIRLIGAF--CPALVYTNLTFSSEAPLRTGLEL--LQDIDSLDT 688
 DB 70 MMGRLRMKRNKSGLVIIIGILPISILSLEFKN--KDDMPYMSQAOEIHQEKAEER 125
 OY 689 EKSPLYGQSRHELEVAAPRAQGDG-----PRAVLLTRMKKFKCAPVTVLGL 737
 DB 126 EKPTKEKEEDDELTAALGRNNGESSRKDEEVOSKRLLPGLKRIEFPNAPVYKWP 185
 OY 738 NVWVFAFLFTTYVLYVDFRPPPOGSPGSEVTLVFWFTVLVEIRIOGFTDEDTLHV 797
 DB 186 YTLAVIGTLMFNIVLVKME--RWPTQGVIVSYFTLIGIKRKE--ILMSEPKLIQ 241
 OY 798 KFTLVGNMKNKCDNVAIFLPIVGTGCMLEPSAFEA--GRTVLADFNWFTLRLIHIFAIH 856
 DB 242 KVKWMLQEVWVNTDIALILLESVGMILRLQDPFRSDGRVIVCVIIYWIYRLDIFGVN 301
 OY 857 KOLGKIIIVRRMMDVFFPLFLFSLVWLVAVGTTQALLHPHDGLBEMIFRVLVRYPLQ 916
 DB 302 KYLGIVYVMIGKMDMMIVYIYLVMSFGVARQALLFPVEEBSMKLAKNIFFMPYWM 361
 OY 917 IFGQIPLEIDEARVNCSTHPLLEDS-----PSCPSLYANWLVILLVTFELVTVNVLM 971
 DB 362 IYGEVFAQIDPPGQGNTR---EDGKITIQPKCT--GANVIYAINACVILVANNILV 415
 OY 972 NLLIMSEYTTQOVVGNATMFKFORVNLIVYEHRRPALAPPFILSHLSLTLRRVFKKE 1031

DB 416 NLLAVENNTEFEVKSJNSQVWKFQRYQLINTFERPVLPPLLIIFSHMTMI PQHLCGRW 475
 OY 1032 AEHREHLERD-----LPDPLDQVVTWETVQKENFLSKMEKRRRDEGEVLRTAHRY 1085
 DB 476 RKHSDDPDERYGLKFLITDELKKVHDFEQCCIEYREDDDFNSNDRIRITSRY 535
 OY 1086 DFIKTYGGLREQERIKC-----LESQINYSVLVSSVADYLAQCG-----PRS 1131
 DB 536 ENMSMRLEEVRRHSMKASIQTVDIRLAQLEDLIGMATALERTLUTGERAESNKIRSR 595
 OY 1132 SQHCGEGSLV 1142
 DB 596 SSDCTDAAYIV 606
 RESULT 3
 TRP_DROME
 ID TRP_DROME STANDARD, PRT; 1275 AA.
 AC P19334;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Transient receptor potential protein.
 GN TRP.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 RX MEDLINE=90180449; PubMed=2516726;
 RA Montell C., Rubin G.M.;
 RT "Molecular characterization of the Drosophila trp locus: a putative
 RL integral membrane protein required for phototransduction."
 RL Neuron 2:1313-1323(1989).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90148782; PubMed=2482778;
 RA Wong F., Schaefer E.L., Roop B.C., Lamendola J.N., Johnson-Seaton D.,
 RA Shao D.;
 RT "Proper function is important for normal visual transduction in the
 RT adult."
 RL Neuron 3:81-94(1989).
 [3]
 RP SEQUENCE OF 1126-1275 FROM N.A.
 RX MEDLINE=88042982; PubMed=3118483;
 RA Wong F., Yuh Z.T., Schaefer E.L., Roop B.C., Ally A.H.;
 RT "Overlapping transcription units in the transient receptor potential
 RT locus of Drosophila melanogaster."
 RL Somat. Cell Mol. Genet. 13:661-669(1987).
 CC -1- FUNCTION: REQUIRED FOR PHOTOTRANSDUCTION. SUGGESTED TO MEDIATE
 CC CALCIUM ENTRY. SEEMS TO FORM A LIGHT-SENSITIVE CALCIUM PERMEANT
 CC CHANNEL.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE RHABDOMERIC
 CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
 CC SUBFAMILY.
 CC -1- SIMILARITY: Contains 2 ANK repeats.
 CC -----
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 CC -----
 DR EMBL; M34394; AAA28976.1; -.
 DR EMBL; M21306; AAA56928.1; -.

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DR EMBL; M18634; AAA28977.1; -.
DR FlyBase; Fggn0003861; trp.
DR GO; GO:0016028; C:ribosome; IDA.
DR GO; GO:0008377; P:light-induced release of calcium, from inte. .; IDA.
DR GO; GO:0009416; P:response to light; IMP.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel - TrpL.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR002153; Trans receptor.
DR InterPro; IPR004729; Trp_Catchannel.
DR Pfam; PF00023; ank; 2.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PRO1097; TRANSRECEPT.
DR SMART; SMO0248; ANK; 2.
DR TIGR; TIGR00870; trp. 1.
DR PROSITE; PSS0088; ANK_REPEAT; 1.
DR PROSITE; PSS0297; ANK_REGION; 1.
DR Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW Vision; ANK repeat; Repeat.
FT DOMAIN 1 366 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 367 387 POTENTIAL.
FT TRANSMEM 388 390 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 391 411 POTENTIAL.
FT TRANSMEM 412 418 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 419 439 POTENTIAL.
FT TRANSMEM 440 450 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 451 471 POTENTIAL.
FT TRANSMEM 472 507 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 508 528 POTENTIAL.
FT TRANSMEM 529 541 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 542 562 POTENTIAL.
FT TRANSMEM 563 638 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 639 659 POTENTIAL.
FT TRANSMEM 660 1275 EXTRACELLULAR (POTENTIAL).
FT REPEAT 69 98 ANK 1.
FT REPEAT 143 172 ANK 2.
FT REPEAT 285 288 GORO -> ASSE (IN REF. 2).
FT REPEAT 326 329 RRKO -> POE (IN REF. 2).
FT REPEAT 365 374 KPFVKFTHS -> NPSSSRTP (IN REF. 2).
FT REPEAT 785 785 S -> N (IN REF. 2).
FT CONFLICT 785 785
SQ SEQUENCE 1275 AA; 142589 MW; 91CFCD9896989B1 CRC64;

Query Match 5.2%; Score 318; DB 1; Length 1275;
Best Local Similarity 19.9%; Pred. No. 3e-13;
Matches 183; Conservative 133; Mismatches 276; Indels 328; Gaps 39;

274 VPKVAEK-QPKKPKSGHSMEDIVRWTKLQNIHSH-----QHLLTYDFPEQEGS 323
48 VKKILEYQGTDFK---NINCTDPMNRSAISAIENENFDLAVILLEHNIIEVDALLHAI 104
324 EELDTYILKALVAKCKSHSEPDYDELKLAVAMRVDAKSEIFNGDVEMKSCDLEEV 383
105 SEEYVAEVELLQWETNHEGQPY-----SWEAVDSKS-TTVVDI-----TP 147
384 MYDALVSNKEPFLFVDNGA-----DVADFLTYGRLO-ELYRSVSR 424
148 LILAAHRNNVEILKILDRGATLPMRHVYKCGDECYTSOTTSLSHSGRIAYATLSA 207
425 KSLFLDLQKQSEARITLGLTQQAAREPPAPPAFSLHEVSRLK--DFLODACKRGFY 482
208 SSLI-----ALSSRD-----PVLTVQLSMELKRLQAMESSEFRAEY 243
483 QDGRPDGRRAEKGPARKPTGCKMLDINKSENPMRDFLMNAVLDNRHEMATYFWAMQ 542
244 TEMR---QWQDFGTS-----LIDHARTS-----MELEWMLFNHPSHDICLQ 286
543 EGVAALAAACKILKEMSHLETEAARATREAKYERLALDLFSECVNSSEARAFALLVR 602
287 -----KQTLER----- 292
603 NRCWSTKTCGLHATEADAKAFPAHDGVAFLTRIWMGDMAAGPILRLGALCPALVYT 662
293 -----LKLAIKYQKTFVAHPNVQQLAAIWD---GHPGFR----- 326

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OY 663 NLITFEAPRTGLELDQDLSIDTEKSPYGLQSRVEELVEAPRAGDGRPAVFLLT 722
DB 327 -----RKQASQQLMDVVKGC-SFPIYSL-----KYLAPDSESG----- 359
OY 723 RWRKMGAPVTVFLGAVNVMYFAFLF-----FYVL--LVDRPREPQG 763
DB 360 --AKFMKRPVKFTHSCSYMFLLMLGMAASLRVQITFELLAPFMWLTJMEDWKBERG 417
OY 764 --PSGEVTLVFWVTVLLEER-----QGFTDEDTLWKKFTLVGDNMKCDVAIFL 817
DB 418 SLPGIELAITTYMALIFEBKSLYSDGLE-----YIMLMNIVDIYSNMF 465
OY 818 FIVGVTCR-----MLPS--AFEGRTVLAMDPMVF 845
DB 466 YVTWLICGATAMVIVHRDLWFRGIDPYPRRHHMHPFDMLLSEGAFAAG-----WVF 517
OY 846 T-LRLIHIFAIHKQIGPKTIIVERMKGVFFFLFSLVLAAYGTTQALL----- 895
DB 518 SYLKLVIHFSINPHLGPIQVSLGRMIIDIIKFFFIYTLVLAFAFGGLNQLIMVALEKN 577
OY 896 ---HHDRLEW-----IFRRV--LYRP-----YLDIFQIPLDEIDEARVNCSTPL 938
DB 578 KCYHLHPDVADPDQEKACTIWRFRSNTFETQSIFWASFGVLVDSFDLAGINS----- 632
OY 939 LLEDSPSCPSLYANMLVILLVTFPLVTNVLMLMLIMFSYEQVVOGNATMFWKFOR 998
DB 633 -----FTRWALMGSGSYVINIYVLNMLIMNSVYIISERADTEKFAFS 681
OY 999 NLIIVEYHE-RPALADPFLSHLSTLRRVFEKEAHEKREHLERDL--PDLQCVYTW 1055
DB 682 QLMMSYFPGDGTIPPEFNLCPNMKMLRKTGLKRPSTRTKSPFKRSKMERACQTLHDKVM--- 738
OY 1056 TVQKENFLSKMKEXRRRDESG 1075
DB 739 KLVRRYIT-AEQRRDDYG 757

RESULT 4
CELL_CAEEL STANDARD; PRT; 1418 AA.
ID CELL_CAEEL
AC P34641;
DT 01-FEB-1994 (Rel. 28; Created)
DT 01-FEB-1994 (Rel. 28; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Ced-11 protein.
GN CED-11 OR ZK512.3
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodetidae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Lathille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy K., Rifkin L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smalton N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL Nature 368:32-38(1994).
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RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spreading A.C., Stapleton M., Strong R., Sun E.,
RA Svetkey R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of *Drosophila melanogaster*.";
CC Science 287:2185-2195(2000).
CC -1- FUNCTION: BINDS CALMODULIN. SUGGESTED TO MEDIATE CALCIUM ENTRY.
CC SEEMS TO FORM A LIGHT-SENSITIVE CALCIUM PERMEANT CHANNEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE RHABDOMERIC
CC MEMBRANES OF THE PHOTORECEPTOR CELLS.
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -1- SIMILARITY: Contains 2 ANK repeats.
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CC -----
DR EMBL: M88185; AAA28979.1; -.
DR EMBL: AE003832; AAM68793.1; -.
DR PIR: JH0588; JH0588.
DR GO: GO:0016021; C: integral to membrane; NAS.
DR GO: GO:0016029; C: rhodome; IDA.
DR GO: GO:0015075; F: ion transporter activity; NAS.
DR GO: GO:0009628; P: response to adrenergic stimulus; IMP.
DR InterPro: IPR002110; Cat channel_TrpL.
DR InterPro: IPR005821; Ion trans.
DR InterPro: IPR005820; M+channel_nlg.
DR InterPro: IPR002153; Trans_receptor.
DR InterPro: IPR004729; Trp_CatChannel.
DR Pfam: PF00023; ank; 2.
DR Pfam: PF00520; ion_trans; 1.
DR PRINTS: PRO1097; TRANSRECEPTR.
DR SMART: SM00248; ANK; 2.
DR TIGR: TIGR00870; trp.1.
DR PROSITE: PS50088; ANK_REPEAT; 1.
DR PROSITE: PS50297; ANK_REPEAT_REGION; 1.
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW Calmodulin-binding; Vision; ANK repeat; Repeat.
FT DOMAIN 1 340 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 341 361 POTENTIAL.
FT DOMAIN 362 373 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 374 394 POTENTIAL.
FT DOMAIN 395 431 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 432 452 POTENTIAL.
FT DOMAIN 453 512 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 513 533 POTENTIAL.
FT DOMAIN 534 548 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 549 569 POTENTIAL.
FT DOMAIN 570 645 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 646 666 POTENTIAL.
FT DOMAIN 667 1124 CYTOPLASMIC (POTENTIAL).
FT REPEAT 78 107 ANK 1.
FT REPEAT 152 181 ANK 2.
FT DOMAIN 710 727 CALMODULIN-BINDING (POTENTIAL).
FT DOMAIN 809 825 CALMODULIN-BINDING (POTENTIAL).
FT CONFLICT 228 229 II -> SS (IN REF. 1).
SQ SEQUENCE 1124 AA, 127749 MW, AF6323BA27626583 CXC64;

QY 295 DIVRWTKLONITSHOH-----LTVYDEQEGSEELDTVL-----KALVK 336
Db 53 DMPVNRRLQLKRLRQHININCMDEPLGRALTL-AIDNENLEMVELLVMGVETKDALH 111
QY 337 ACKSKSQEPDYDLKALV-----AMDRVDAKSEIFQNDVWKKSCDLEWVVDALV 389
Db 112 AINAEFVAVELLEHEELLYKEGSPYMWOKVDI-NTMFAFDI-----TPMLLAH 162
QY 390 SNKPEFVLEVDNGA--DVADFLTYGRLOELYRSVRKSLFDLLQRKQEARLTLAGIG 447
Db 163 KNKFEILILDLGRGAAYVPHDIRG-CECYRLTAESL-----RHSLSVN 209
QY 448 TQOAREPP-----AGPAFSLHEVSRVKD--FLQDACRGFYQGRPDGRRRAEKPAK 499
Db 210 IYRALCPSLLCLTSDNPLITFAQLSWELRNALTEQCKSEYMD-----LRQCKFAVD 265
QY 500 RPTGQKMLDLNOKSENWRDLFLMAVYQNHENATYFMWQGEVAAALAAKLIKMS 559
Db 266 -----LIDQRTSNE-----LAILIYDPOWSSY-----EPG----- 292
QY 560 HLETAAABATREAKYERKALDLFSECCYNSSEARAFALVRRNCWSEKTTCLHATEAD 619
Db 293 -----DRMSL-----TRVQAISYK 307
QY 620 AKAPFAHDGVQAFLTRIMWGMAACTPILR--LIGAFLCFALVYTNLITFSEAPLRFG 676
Db 308 QKKFAHNIQQLSSIYVD--GLPGRRSYIDVKICIAOV--AVLF----- 351
QY 677 LEDLDDLSLDTKSPLYGL-----QSRVELVAPPAQDGRGRAVFLTRMKPFMGA 730
Db 352 -----PLVCLIYMCAPNCRGTQLM-----RK----- 372
QY 721 PVTVELGNVWVFAFLPLFTVLYL-----DFRPPQSPG 766
Db 373 PFMKFLIHASSTYLFLEF--LILVSGQADDDFVRIFGTRMKKELAEOLRQOTBSK 429
QY 767 PEVTLVFWVFLVLEIRQGFETDEDTHLYKKFTLYVGDNNKCDMVAIFLEIVGTCRM 826
Db 430 LELIVMVYVIGFVMEVQEIFAVGMS-----YLRNMNVFIDFLRNSLY-VGVMC-L 479
QY 827 LPSAFEGRTVLAMD-----FMVTT-LRLHIFAIHQOL 859
Db 480 RAFAYIQOATEIARPOWAVYIPREKMHDPQLIAEGFAANVVSARKLVLFSLNPL 539
QY 860 GKLIIVRRMKDV--FFFLPFLSYMLVAAYGT-----TQALLHPDGLW-- 904
Db 540 GFLQSLGKMWVIDVYKFFFTYTLVFAFACGLNQLMTFALEKSKCYLP-GSEADMS 598
QY 905 -----IFRRV--LYRP-----YLQIFQOIPLDEIDEARVNCSTHPLLEDSPSCPSLYAN 952
Db 599 HGDSCMKRRRPNLESSQSJFWASFVGVGLDDFLSGIKS-----YTR 642
QY 953 WIVILLVTELLVNLVNLMLLIAMFSTFPVQGNATFMKFORXNLYVEHPRP-LA 1011
Db 643 FGLMLFGSYVINIYVNLILMIAMMSYAMIDHSPTWFAFTKLMGSEFBSATLP 702
QY 1012 PFIILSHSLRLRVEFKKAHREHLEHRLDPDLQKVYVWEVQENFYSKMEKRR 1071
Db 703 PFENVLPYKQVI-RIFRSS-----KTIIDQRSKKRKEQOF 739
QY 1072 DEGEVLRKTAHRVDPIAKYLGLEQO-----EKRIKLESQIN 1110
Db 740 SEYDNIMR-----SLWRYVAAMRKRENNVSEDDINEVSEIN 779

RESULT 6
TRP2_MOUSE
AC Q9R244; Q9R244; Q9R244; Q9R243; PRT: 1172.AA.
DT 16-OCT-2001 (Rel. 40). Created
DT 16-OCT-2001 (Rel. 40). Last sequence update
DT 28-FEB-2003 (Rel. 41). Last annotation update

DR	PRODOM	P0023136	Xrccl_N, 1.
DR	SMART	SM00248	ANK, 2.
DR	PROSITE	PS50088	ANK REPEAT; FALSE NEG.
DR	PROSITE	PS50297	ANK REP REGION; FALSE NEG.
KM	Ionic channel	Transmembrane; Ion transport	Calcium channel;
KM	ANK repeat	Repeat	Alternative splicing
FT	DOMAIN	1	659
FT	TRANSNM	660	680
FT	DOMAIN	681	702
FT	TRANSNM	703	723
FT	DOMAIN	724	738
FT	TRANSNM	739	759
FT	DOMAIN	760	789
FT	TRANSNM	790	810
FT	DOMAIN	811	833
FT	TRANSNM	834	854
FT	DOMAIN	855	899
FT	TRANSNM	900	920
FT	DOMAIN	921	1172
FT	REPEAT	301	330
FT	REPEAT	377	406
FT	REPEAT	430	459
FT	DOMAIN	1140	1143
FT	VARSPLIC	1	111
FT	CONFLICT	628	628
FT	CONFLICT	633	633
FT	CONFLICT	653	653
FT	CONFLICT	774	774
FT	CONFLICT	797	797
FT	CONFLICT	1161	1161
FT	SEQUENCE	1172 AA	130467 MW; B6E6F4B8941E946 CRC64;
Query Match		4.2%;	Score 258.5; DB 1; Length 1172;
Best Local Similarity		20.2%;	Pred. No. 2.7e-09;
Matches	239;	Conservative	144; Mismatches 364; Indels 439; Gaps 51
OY	161	HYPR--DDGSGG--PLC----	SIDSNSHFLVEPGP--PGKGDGTELRRLRK 206
DB	215	HRPQTKSDGGGVQAAGCPICAGFFSITTL	PQHNATCGESPPPOASPASLSSSESVLR 274
OY	207	HISGRACGYGSGSIEIFVCLLVNGDPN	TLERISRAVEQAAPMLILVSGSIGIADVLAAL 266
DB	275	H-----HVALTPVLPVLPKPNNWTE-----	-----I 295
OY	267	VNOEHLVPRVAEKQFEKFKPSKAFS	WEDIVRMTKLONTSHOHLTVVDFEOGSEEL 326
DB	296	VNK-----KLKFP-----PTLRAL-----	-----QEGQLG 317
OY	327	DTVLKALVAKS-----HSGEODYL	DELKLVAVMDRYDIASKEIFNGDVEWKS 377
DB	318	VQQLLESPPDASGAGPGPLANVESE	SDRSREALNLAIRLGHEVI--TDVLANVKPDE 375
OY	378	CDLEEWAVDALVSKKEPEFVRLFV	UNGADVADFLTYGRQ--ELYGSVSKSLF
DB	376	ROIHEALLVAADTQAPVVRRLT-----	ARLEREKGRVDTKFSFLAFDDSI 423
OY	437	EEAR-----LTLAGGTQOARPR	PAGPRAFSLHEYSRVLKDELDAACRGFY
DB	424	DGSGFAGCVTPFLTACQK-----	DLYEAOILMDGSHITAR-----PHVSCAC 467
OY	493	AEKGPARKPTGQKLLDLNOKSEN	PWDRFLMAVLQNRHEMATYFMWAGDEGVAAALAC 552
DB	468	LEGNARRYD-----LTKESLSR	INTYTGISRAHSLASE-----DPMIAAF 510

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QY 553 KILKEMSHLETAABATREAKYERIALDLFSECSSEARAPALL--VRNRCSKTC 611
DB 511 QLSRELRL-----ARKEPEKPOYIALESICDY-----GFELMGCRQ--SEVTA 556
QY 612 -----LHATEADAKAFPAHDGQAFLETRIMWD 640
DB 557 VLNDGDESETEREABAGLQAFEEGIPNARLARLVNYYQGFVAHPICQVLAISIMGN 616
QY 641 MA---AGPITLALGA-----FLCPALVYTNLTTSSEAPLRTGLEDDLDLSLDE 689
DB 617 LAGMRGSTITMRLFVASLIFLTMPLFCIG----- 645
QY 690 KSPILGLOSREVELVEAPRAGDRGRAVELLTRMKFWDVTVLGNVYVAFPL-FL 748
DB 646 ----YWL-----APKSO-----LGRLLKI--PVLKFLHSASYLWFLPL 679
QY 749 FTYVLVLD-----FRPPQSGSGPEVTLV-FWVFTLVLEIRGPFTEDETHLVKFTLY 802
DB 680 LGESLVMETQSTFKGRSQ--SVWETSLHIMVWTGTLMECKEVM-----IEGLREY 729
QY 803 VQDNKKCMVAIFLFTV-----GVTCKMLPSAFEA----- 833
DB 730 LIDMWNFLDVVILSYLASFALRLLAGLVNHCRRDASDSTTCRCFTTARSEMRTEPO 789
QY 834 --GRITLAMDVWFTLRLHIFAIHQGLPKIIVERMKKGVFFFLFSLVWLVAVGVT 891
DB 790 FLAEVLFVTSMLSTFKLAVIILPAHESLGLTLOISICKMDMTRFVILMITLTLAFLGL 849
QY 892 QALLPHD-----GRLEWIFRRVLYKRYPLQIFQOPLDEIDEARVNCSTHPLLEDSPSC 946
DB 850 NNIVYVQSEKLGNNENEFQFLW-----TWFQMEHETVD-----MPQFLVEFVG 897
QY 947 PELVYANWVILLVTLVTLVNLVNLVNLVNLVNLVNLVNLVNLVNLVNLVNLVNLV 1005
DB 898 RMYGIFITVWVIV-----LNMILTAMITNSFOKIEDADVWKFARSKLYLSYER 948
QY 1006 EEPALAPFLILSHSLT--LRVFK-----KEA 1032
DB 949 EGTLPFPVNNILSPAPAFYLVRIFRPLCCSSCKKAKSDYPPGTITNGARAGSAG 1008
QY 1033 EHKREHLERDLDPDLQKVTVETWQENFLSMKERRRDESEGVLRKTAHRVDFLAKYL 1092
DB 1009 EGERVSYRRLVYKALVQRYI--ETARE-----FEETRR-----KOL 1043
QY 1093 GG-LRQERIKICLESQINYCVLVSADVLAQGGGPR-----SSQH 1134
DB 1044 GRLTELTKTVSRLOSE-----VASVQKNILAGAGAPRPDASILSRVITRVNSFQ 1096
QY 1135 CGEGSQLVADHR-----GGIDGWBQGA---GPPSDT 1165
DB 1097 LGPPTSDTPAELTMPEIVETEVS LGDGLDGTGEAGAPARPEPSSS 1142

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RT RESULT 7
TRP2 RAT STANDARD; PRT; 885 AA.
AC Q9R283;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Short transient receptor potential channel 2 (TrpC2) (TRP2).
GN TRP2 OR TRP2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=99254120; PubMed=10318963;
RX Litan E.R., Corey D.P., Dulac C.;
RT "TRP2: a candidate transduction channel for mammalian pheromone
sensory signaling.";

```

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RL Proc. Natl. Acad. Sci. U.S.A. 96:5791-5796(1999).
CC -! FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED CALCIUM PERMEANT
CC CATION CHANNEL. PROBABLY IS OPERATED BY A PHOSPHATIDYLINOSITOL
CC SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR TYROSINE KINASES OR
CC G-PROTEIN COUPLED RECEPTORS. IS NOT ACTIVATED BY INTRACELLULAR
CC CALCIUM STORE DEPLETION.
CC -! SUBCELLULAR LOCATION: Integral membrane protein (probable).
CC -! TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN VOMERONASAL ORGAN
CC NEURONS (SENSORY MICROVILLI).
CC -! SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUPERFAMILY.
CC -! SIMILARITY: Contains 3 ANK repeats.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, AF136401; AAD31453.1; -.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR005820; M-channel_nlg.
DR InterPro; IPR002153; Trans_receptor.
DR InterPro; IPR005458; Trpchannel2.
DR Pfam; PF00023; ank; 2.
DR Pfam; PF00520; Ion_trans_1.
DR PRINTS; PR01097; TRANSRECEPRP.
DR PRINTS; PR01643; TRPCHANNEL2.
DR SMART; SM00248; ANK; 3.
DR PROSITE; PS50068; ANK_REPEAT; FALSE NEG.
DR PROSITE; PS50297; ANK_REPEAT_REGION; FALSE NEG.
DR Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW ANK repeat; Repeat.
FT DOMAIN 1 375 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 376 396 POTENTIAL.
FT DOMAIN 397 418 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 419 439 POTENTIAL.
FT DOMAIN 440 454 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 455 475 POTENTIAL.
FT DOMAIN 476 505 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 506 526 POTENTIAL.
FT DOMAIN 527 549 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 550 570 POTENTIAL.
FT DOMAIN 571 615 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 616 636 POTENTIAL.
FT DOMAIN 637 885 CYTOPLASMIC (POTENTIAL).
FT REPEAT 17 46 ANK 1.
FT REPEAT 93 122 ANK 2.
FT REPEAT 146 175 ANK 3.
FT DOMAIN 853 858 POLY-SER.
SQ SEQUENCE 885 AA; 99611 MW; BA23F87F2BEFA85 CRC64;

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Query Match 4.0%; Score 244; DB 1; Length 885;
Best Local Similarity 21.2%; Pred. No. 1.7e-08;
Matches 192; Conservative 121; Mismatches 301; Indels 290; Gaps 37;
QY 344 EPQDYLDLKLAVANDRVDAIKSEIFNGDVWKSCLDEWVDALVSNKPEFVRLFDVNG 403
DB 60 EDRSWREALNLAIRLGHEVI--TDVLNVNKKDPFQIHALLAVADTNGPAVVRRL--- 114
QY 404 ADVADFLTYGRQ-ELYRSVSKSLFDLLQKQEBAR---LTLAQLCTQQAAREPPAGP 458
DB 115 -----ARLEREKGRKVDTKSFLAFDSDSISGSRAPVTPVTLAQR----- 157
QY 459 PAFSLHEVSRVVKDPLQDRCRGFYODGRGRARRAKRPTQGWLLDNLQSENPM 518
DB 158 --DLYETALQLMLMDGHTTAR-----PHPVSCACLECSNARYD---LLKFSLSRINTY 205
QY 519 RDLFLVAVLQNHENATYFWAMGQGVAAALAAKILKEMSHLETAABATREAKYER 578

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Db      206 RGIASRAHSLASE-----DMILAIFOLURELRRL-----ARPEPEKQY 246
Qy      579 LALDIFSECYNSSEARAFALL-VRNRRCWSKTT-----611
Db      247 IALSELCDY-----GFELGMCNQ--SEVTAVLNDIGSESEPEAEGLQAFEEGI 298
Qy      612 ----LHATEADAKAFPAHDGVQAFTRIMWGMA--AGTPIRLGALCFALVYTN 663
Db      239 PNLARLRLAVNYNQOFVAPHICQOVLSSIMCGNLAGMGRSTTIWKLFWAFILF-LTWP 357
Qy      664 LITFEEDAPLRGTGLDLDLSDLTREKSLVGLQSRVELVAPRAQGRGRAVFLTR 723
Db      358 LCTGYWLP-----KSRLLGLK-----375
Qy      724 WRKFWGAPVTEFLGNVVMYFAFL-FLFTYVLVD-----FRPPQPSGSEVTLV-FWVF 776
Db      376 ----IYVLRKLHLSASTLWFLFLGLGSLVMEQLSTFKRSQ--SWETSLSMIVYT 427
Qy      777 TLVLEIRIGGFTEDETHLVKKFTLVYVGDNNKCDMVALFLFVGV-----822
Db      428 GFLEWCEKEVW-----IEGLRSYLLDMNFDVILSTVLASFALRLLAGLAWMC 479
Qy      823 ----TCRMLPSAFEA-----GRVLANDFMVFTLRLLHIFAIHKQLGPKIIV 865
Db      480 RDASDSSTCRYFTTARSEMRTEDEPLAEVLFVAVTSMLSFTRLAYILIPAHESLGLQIS 539
Qy      866 VERMMKQVFFLFLFVSVMLVAVGTTQALLHPD-----GRLEWIFRRLVAPYVQIQG 920
Db      540 IGMKMDMIRFWMILMITLTAFLCGLNINIVYQETEKGNENETFOFQFW---TWGMC 595
Qy      921 IPLDEIDARVNCSTHPLLEDSPSCPSLYANMLVLLVFLVTLVTVNLLNMLLJAMESY 980
Db      596 EESHVVD-----MPQFLVEPFGVAMYGIFITVMIV-----LNLMLLMTN 638
Qy      991 TPQVQGNATMFKQRYNLYEY-HERPALAPFLLSHSLT---LRRV-----1028
Db      639 SFQKIEDADAVEMKPARSKLYSTFREGTLTPVPNNILPSPKAFYLLRRIRFPCGS 698
Qy      1029 ----KKE-----AEHKREHLRDLDPDLQKVVTWQCKENLSKME 1067
Db      699 CCKAKKSDYPIPTTNGARAGPBGGEVSYRLRYTALVQRYI--ETARE-----FE 751
Qy      1068 KRRDSEGEVLKTAHRYDIFAKYLG-LREOEKIKLESQINCSVLSVADVLQAG 1126
Db      752 ETRR-----KDLGNRLTELTKVSRQSB-----VASQKTVAG 786
Qy      1127 GQPR 1130
Db      787 GALR 790

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RESULT 8
TRPL_CAEEL STANDARD; PRT; 1027 AA.
AC P34586; P34586; O81G03;
DT 01-FEB-1994 (Rel. 28, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transient-receptor-potential like protein (TRP homologous cation
channel protein 1).
GN TRP-1 OR STRPC1 OR ZC21.2/ZC21.1.
OS Caenorhabditis elegans.
OC Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditya; Metazoa; Pelodermata; Caenorhabditis.
OK NCBI_taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Hareneck C.; Schults G.;
RT "Cloning and functional expression of C. elegans TRP isoforms.";
RL Submitted (MAR-2000) to the EMBL/Genbank/DBD databases.
RP [2]
RP SEQUENCE FROM N.A.

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RC STRAIN=Bristol N2; PubMed=7906398;
RX MEDLINE=94150718; Anderson R., Baynes C., Berke M.,
RA Wilson R., Almscough R., Anderson R., Copey T., Cooper J., Coulson A.,
RA Bonfield J., Burton J., Connell M., Covey T., Fraser A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser J.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Lattelle P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smailson N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Suleton J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL Nature 368:32-38(1994).
RN [3]
RP REVISIONS.
RA Waterston R.;
RL Submitted (DEC-2002) to the EMBL/Genbank/DBD databases.
CC -1- FUNCTION: COULD MEDIATE CALCIUM ENTRY AND FORM A CALCIUM PERMEANT
CC CHANNEL (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -1- SIMILARITY: Contains 3 ANK repeats.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: AJ276027; CAC81654.1; -
CC EMBL: L16685; AAC28167.3; -
CC WormPep; ZC21.2; CE33009.
CC InterPro: IPR002110; ANK.
CC InterPro: IPR002111; Cat_channel_Tyrl.
CC InterPro: IPR005821; Ion_trans.
CC InterPro: IPR002153; Trans_receptor.
CC InterPro: IPR004729; Trp_Channel.
CC Pfam: PF00023; ank; 2.
CC Pfam: PF00520; ion_trans; 1.
CC PRINTS: PR01097; TRANSRECEPT.
CC SMART: SM00248; ANK; 2.
CC TIGRFAMs: TIGR00870; trp; 1.
CC PROSITE: PS50088; ANK_REPEAT; 1.
CC PROSITE: PS50297; ANK_REPEAT_REGION; 1.
CC Hypothetical protein; Ionic channel; Transmembrane; Ion transport;
CC ANK repeat; Repeat.
CC ANK repeat; Repeat.
CC TRANSMEM 355 375 POTENTIAL.
CC TRANSMEM 391 411 POTENTIAL.
CC TRANSMEM 473 493 POTENTIAL.
CC TRANSMEM 516 536 POTENTIAL.
CC TRANSMEM 559 579 POTENTIAL.
CC TRANSMEM 640 660 POTENTIAL.
CC REPEAT 85 115 ANK 1.
CC REPEAT 117 141 ANK 2.
CC REPEAT 153 192 ANK 3.
CC SEQUENCE 1027 AA; 118101 MW; E1B83635A5DE2PAD CRG64;

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Query Match 3.9%; Score 239; DB 1; Length 1027;
Best Local Similarity 19.5%; Pred. No. 4.5e-08;
Matches 134; Conservative 109; Mismatches 234; Indels 210; Gaps 25;

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Qy 549 LAACKIKEMSHLETEAARAT---REAKYERLALDFSCYNSSEARAFALLVRRNR- 604
Db 240 LSAFLSMDLQRLAFEEHEFETLYLOLSECKQYSCDLSGCRSSE--VAILNKGNV 297
Qy 605 ----CMS---KITCLHATEADAKAFPAHDGVQAFTRIMWGMAAGTPIRLGAF 655

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Db 298 NDNNDIVWASKLSLSRLKLAIEQKAFVSHPHCOOLLTSIYW-----ESIPYRORSQTWA 353
Qy 656 CFAIYVNTLITSESEAPLRTGLEDJODDLSLSTKESPLVGL-----GSRVELVEAPRA 709
Db 354 NEFLAFLFLM-----PIFCMLYILMPKSLRLGLRVSP-- 387
Qy 710 QCDRGPRAFVLLTRMKFWGAPVTVFLGNVVMYFAVLFPLFTVLLVDF-----R 758
Db 388 -----FMKFFYYSVS-----FATFLGLLTATPEFDYVEKGERGMTR 425
Qy 759 PPPQSGSP--EVLTYFWVFTVLEIRGQFTDEDTLVKKFTLYGVGNMKCDMAVIF 816
Db 426 ASDRGPRATWVESLVFTWVIGMLMSEIRKQLM-----EEGFKRYMRQMMWMLFLMIC 477
Qy 817 LEIVGTCMLPSAPF-----AGRTVAMDFWFTLRLLHI 852
Db 478 LVLCTISIRL--SAYITFYREDPRYRTVRYTWTSEPMVAAPALFAVGNVSPFAITYL 535
Qy 853 FAIHKQLEKRIIVEREMKDVFFLFELSVLWVAVGTVTQALLPHPDGLLEWIFRRLVYR 912
Db 536 FQTNPYLGPLOISLGLMVDVAKFCIFVLIISSPSIGLAQLWYVDPTDVCLEPATCK 595
Qy 913 PVLQIFGQIPDEIDEARVNCSTHPLL-----EDSPSCPS-LVANMLVILLVTF 962
Db 596 HSNVFFSSI-----ADSYLTLSLFSITKPEDTDVVENHKITQWVGQGFIMY 644
Qy 963 LLVTNVLNLLIAMSTYFQVVGQATPMFKFORNL-IVEYHERPALAPF-ILSL 1020
Db 645 HCTSIIVLLNMLIAMSHSFQIINDHLEWKFHRTKLMAMHDESSLPFPNIIIVTK 704
Qy 1021 SL-----TLRVFKKEA-----EHKREHLER-----DLPPPLDQK 1050
Db 705 SLIYVNCLEFNIVRWMLGKYTKYQKNRATIRPGVSRGNEMKSGCHDDSLKPLTYA 764
Qy 1051 VVTWETVQ-----KENFLSKMEKRROSEGEVLKRTARVDF 1087
Db 765 DIITTLVAFIRHQTKKMDKMGVNEEDLHEIKODISLREYLRDDRREIVRSSSH-IDA 823
Qy 1088 IAK-----YLGSLRQEKER 1101
Db 824 VRDIDWRITWTSSTRPREGSMRLPKTR 850

RESULT 9
TRP5_HUMAN STANDARD; PRT; 973 AA.
ID TRP5_HUMAN Q9UL62; Q9Y514;
AC Q9UL62; Q9Y514;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Short transient receptor potential channel 5 (TRPC5) (Htrp-5) (Htrp5).
GN TRPC5 OR TRP5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID:9606;
RN [1]_TaxID:9606;
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=99425273; PubMed=10493832;
RA Sossaye-Alaoui K., Lyon J.A., Jones L., Abidi F.E., Hartung A.J.,
RT Hane B., Schwartz C.E., Stevenson R.E., Srivastava A.K.;
RT "Molecular cloning and characterization of TRPC5 (HTRP5), the human
RT homologue of a mouse brain receptor-activated capacitative Ca(2+)
RT entry channel."
RT Genomics 60:330-340(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Rohlfing T., Langston Y., Mead K., Bird C.;
RL Submitted (JUN-1998) to the EMBL/Genbank/DBD databases.
CC -!- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE
CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR

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CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN
CC SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY). MAY ALSO BE
CC ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.
CC -!- SUBUNIT: INTERACTS WITH NHERF (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (probable).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN BRAIN WITH HIGHER LEVELS IN FETAL
CC BRAIN.
CC -!- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -!- SIMILARITY: Contains 2 ANK repeats.
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CC -----
CC EMBL, AF054568; AAF00002.1;
CC EMBL, AC005191; AAC24563.1;
CC EMBL, AL049563; CAB44737.1;
CC Genew; HGNC:12337; TRPC5.
CC MIM; 300334;
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0015279; F:score-operated calcium channel activity; TAS.
CC GO; GO:0006816; P:calcium ion transport; TAS.
CC GO; GO:0007399; P:neurogenesis; TAS.
CC InterPro; IPR002110; ANK.
CC InterPro; IPR002111; Cat_channel_Tyrl.
CC InterPro; IPR005821; Ion_trans.
CC InterPro; IPR002153; Trans_receptor.
CC InterPro; IPR004729; Trp_CaChannel.
CC InterPro; IPR005461; TrpChannels5.
CC Pfam; PF00023; ank; 2.
CC Pfam; PF00520; Ion_trans; 1.
CC PRINTS; PRO1097; TRANSRECEPTR.
CC PRINTS; PRO1646; TRPCCHANNELS5.
CC SMART; SM00248; ANK; 2.
CC TIGRFAMs; TIGR00870; trpf_1.
CC PROSITE; PS50088; ANK_REPEAT, FALSE NEG.
CC PROSITE; PS50297; ANK_REPEAT_REGION, FALSE NEG.
CC Ionic channel; Transmembrane; Ion transport; Calcium channel;
CC ANK repeat; Repeat; Glycoprotein.
CC DOMAIN 1 330
CC TRANSMEM 331 351 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 352 398 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 399 419 POTENTIAL.
CC DOMAIN 420 437 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 438 458 POTENTIAL.
CC DOMAIN 459 470 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 471 491 POTENTIAL.
CC DOMAIN 492 512 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 513 533 POTENTIAL.
CC DOMAIN 534 603 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 604 624 POTENTIAL.
CC DOMAIN 625 973 CYTOPLASMIC (POTENTIAL).
CC REPEAT 629 98 ANK 1.
CC REPEAT 141 170 ANK 2.
CC SITE 971 973 ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN
CC (BY SIMILARITY).
CC CARBOHYD 461 461 N-LINKED (GLCNAC... ) (POTENTIAL).
CC SEQUENCE 973 AA, 111411 MW, PBC8CBF17BEA2166 CRC64;

Query Match 3.8%; Score 231; DB 1; Length 973;
Best Local Similarity 21.5%; Pred. No. 1.4e-07;
Matches 140; Conservative 97; Mismatches 232; Indels 182; Gaps 28;

Qy 555 LKEMSHLETEAANAATREAKYERLALLFSCYCSNSEBARALLVRN-----RCW 606
Db 227 LKELSKVNEFEFAEYEEISQOKLPKALLDARSSREIE--IILNHRDDHSEELDPQY 284
Qy 607 SKTCLHLATEADAFAFPAHDGVQAFILRIWGDMAAGTP-----ILRLGAFLCFAL 659

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Db	285	HDLAKLKVAIKYHQKEFVAQPNQOQLLATLWYD----	GFPGMRKGMVWVLTL----	TCMTI	337
Qy	660	VTNLTLTSEEARLRTGLEDLDLSDLTDEKSLYGLQSRVEELVEAPRAQDGRPPANV	719		
Db	338	GF-----LEPMLSTIAVLIPSRNL-GI-----	358		
Qy	720	LITRWRKFWGAPVTVPLGVNVMFAFLPFE---- <td>TVLLVDFRPPQSGGEVITLYFWY</td> <td>775</td> <td></td>	TVLLVDFRPPQSGGEVITLYFWY	775	
Db	359	-----FKKPEPIKICTHASTYLTVFMILLASQHIVRTDLHVQGPFPVWMTLIPWY	411		
Qy	776	FTLVLEIRQ-----GPEFTEDDTLVKKFTLYVGDNNKCDMAVLEFIVGTCMLPSAFE	832		
Db	412	LGFIINGEIKEMMDGFTL-----YIHWNWLMDFANMSLYLATISLKIYAVVKY	460		
Qy	833	AG-----RTVLAMDPMVFTLRLLIHPAIHKQLGPKIIVERMKDVFPP	876		
Db	461	NGSRPREWEMWHPITLIAELFAISNLSLSRLISLFTANSHPGLQISGRMLDLKF	520		
Qy	877	LEFLSVMLVAYG-----VTTQALLMHP-----DQRLMIFPRVLRYRYLOI	917		
Db	521	LFTYCLVLAIFPANGNLQLYFYETRAIDBNCKGIRCEKONNAFSTLF-ETIQSLFWSV	579		
Qy	918	FGQIPDLDEID-BAVVCSTHPILEDSPSCPSLYANWLVILLVTELVTVNVLMLLTA	976		
Db	580	FOLNLLVYTNVAKR-----HE-----FTFVGATMGTTNVISLVLLNMLIA	622		
Qy	977	MFSYFQVQGNATFWKFORYNLIVEY-HERPALAPF-ILLSHLS-ITLRVPFKKAE	1033		
Db	623	MNNSYQULADHADIADEWKFAPRTKLMSYFDEGGTLPPFNIIIPSPSLYLGWFWNNTG	682		
Qy	1034	HREHLERLPPRLDQKVTVWETVQCKENLSKMEKRKRRS-----EGEVLRTAHAVDF	108		
Db	683	PKRD-----PDGR-----RRRNRLRSFTEHNAOSLIIONPHYOEIRNLVXR--Y	724		
Qy	1088	IA-----KYGLGRQOE-KRIKCSLQNYNCVSLVSSVADVLAQGGPRS	1131		
Db	725	VAAIMRNSKTHGTLTEENFKELKODISSRY-----EVLDLIGNRKHPRS	769		

CC	SUBFAMILY.
CC	-I- SIMILARITY: Contains 2 ANK repeats.
CC	-----
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CC	or send an email to license@isb-sdb.ch).
CC	-----
DR	EMBL; AJ006203; CAA06911.1; -
DR	InterPro; IPR002110; ANK.
DR	InterPro; IPR002111; Cat_channel_Tryp.
DR	InterPro; IPR005821; Ion_trans.
DR	InterPro; IPR002153; Trans_receptor.
DR	InterPro; IPR004729; Tryp_CatChannel.
DR	InterPro; IPR005461; TRPChannels1.
DR	Pfam; PF00023; ank; 2.
DR	Pfam; PF00520; ion_trans; 1.
DR	PRINTS; PR01097; TRANSRECEPT.
DR	PRINTS; PR01646; TRPCHANNELS.
DR	SMART; SM00248; ANK; 2.
DR	TIGRFAMs; TIGR00870; trp; 1.
DR	PROSITE; PS00088; ANK_REPEAT; FALSE NEG.
DR	PROSITE; PS0297; ANK_REP_REGION; FALSE NEG.
KW	Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW	ANK repeat; Repeat; Glycoprotein.
FT	DOMAIN 1 330
FT	TRANSMEM 331 351
FT	DOMAIN 352 398
FT	TRANSMEM 399 419
FT	DOMAIN 420 437
FT	TRANSMEM 438 458
FT	DOMAIN 459 470
FT	TRANSMEM 471 491
FT	DOMAIN 492 512
FT	TRANSMEM 513 533
FT	DOMAIN 534 603
FT	TRANSMEM 604 624
FT	DOMAIN 625 974
FT	REPEAT 69 98
FT	REPEAT 141 170
FT	DOMAIN 690 693
FT	SITE 972 974
FT	CARBONYD 461 461
SO	SEQUENCE 974 AA; 111536 MW; 94256E0F2B925316 CRC64;
Query Match	3.8%; Score 231; DB 1; Length 974;
Best Local Similarity	21.5%; Pred. No. 1.4e-07;
Matches 140;	Conservative 98; Mismatches 232; Indels 182; Gaps 28;
OY	555 LKESHSLETEAARATREAKYERFLALDLSECYNSSEAPAFALLVRN-----RCW 606
Db	227 LKELSKVENEKKEAYEEELSQQCKLFADLLDOARSSELE--ILLNRDDHSEELDPOKY 284
OY	607 SKTCCHLATGEADAKAFPHHDGVAFPLRIWMGMAAGTP-----ILRLGAFLGLPAL 659
Db	285 HDLAKLVALKHYOKEVVAQNCQQLATLYTD---GFPCWRKHVNVKL---TCMTI 337
OY	660 VYTNLITFESEAPLRTGLELDLSDLSDEKSPYLGLQSRYEVLVEAPRAQGDRGRAVF 719
Db	338 GF-----LPMLSLAVLIISPSRN-LGL----- 358
OY	720 LITMRKFCGAPVIFLGNNVMYPAFLF---TYLLVDFRRPPPGSGPEVTLYFWV 775
Db	359 -----FIKKPKIKFICHTASVITFLFMULLASQHIVRTDLHVQGPPTVWEWMIIPWV 411
OY	776 FTVLLEEIRO---GFETDEDTHLVKFTLVVGDNWNKCDMVAFLFTVGTGRMLPSAFE 832
Db	412 LGFIWGSIKKNMGCGTFE-----YIHDMNMIMDPANMSLVLTATLSLKVAIVVKY 460

```

QY 833 AG-----RTVLAMFVETLRLIHFAIKHQLGPKIIVERMMKDVFF 876
DB 461 NSGRREWEWMHPTIALALFAISNLSLISLFTANSHPGLQISLGMLDLKF 520
QY 877 LFFLSVWLVAAG-----VTQALLHPH-----DGRLEWIFRRVLYRPILOI 917
DB 521 LFYICVILIAFANGLNQLYFYETETRAIDEPNNCKGRCCKONNAFSTLF-ETLQSLFWMSV 579
QY 918 FQOIPLEID-EARVNCSTHPLLEBSPCSPLXANWLVILLVPLVLTNVLNMLNLA 976
DB 580 FELNLVYTVNVAR-----HE-----FEEVATMGTVNVLVLLMLLA 622
QY 977 MESYFQVQVGNATVFWKFORYNLVEY-HERPALAPF-IILSHLS-ITLRVFEKAE 1033
DB 623 MWNNSYQLADHADIEKFAKTKMWSYDEGTLPPPNIIIPSPKFLYLGWFWNTFC 682
QY 1034 HKREHLERDLPPLDQKVVTWETVCKENFLSKMEKRRDS-----EGVLRKTAHRVDF 1087
DB 683 PKRD-----PDGR-----RRNHLRSFTEHMDSLIONGHQVEVHNLVLR--Y 724
QY 1088 IA-----KYLGLRPGF-KRIKLESQINYSVLSVADVLACGGGRSS 1132
DB 725 VAMIRNSKTNEGTLTEENFKELKODISSFRY-----EVLDDLGNRKQPRRS 770

RESULT 11
TRPS_MOUSE STANDARD; PRT; 975 AA.
ID TRPS_MOUSE Q90X29; Q90WT1; Q90RD4;
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Short Transient receptor potential channel 5 (TRPC5) (Transient
receptor protein 5) (Mtrp5) (trp-related protein 5) (Capacitative
calcium entry channel 2) (CCE2).
GN GN TRPC5 OR TRP5 OR TRPS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98221157; PubMed=9553080;
RA Okada T., Shintzu S., Wakamori M., Maeda A., Kurosaki T., Takada N.,
Imoco K., Mori Y.;
RT "Molecular cloning and functional characterization of a novel
RT receptor-activated TRP Ca2+ channel from mouse brain.";
RL J. Biol. Chem. 273:10279-10287(1998).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20545496; PubMed=10980202;
RA Tang Y., Tang J., Chen Z., Trosc C., Flockerzi V., Li M., Ramesh V.,
Zhu M.X.;
RT "Association of mammalian trp4 and phospholipase C isozymes with a PDZ
RT domain-containing protein, NHERF.";
RL J. Biol. Chem. 275:37559-37564(2000).
RN (3)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98353453; PubMed=9687496;
RA Philipp S., Hambricht J., Braslavski L., Schroth G., Freichel M.,
Mueckel M., Cavaliere A., Flockerzi V.;
RT "A novel capacitative calcium entry channel expressed in excitable
RT cells.";
RL EMBO J. 17:4274-4282(1998).
RN (5)
RP SEQUENCE OF 515-637 FROM N.A.

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RX MEDLINE=96234226; PubMed=8646775;
RA Zhu X., Jiang M., Peyton M., Boulay G., Hurst R., Stefani E.,
RA Birbaumer L.;
RT "trp, a novel mammalian gene family essential for agonist-activated
RT capacitative Ca2+ entry.";
RL Cell 85:661-671(1996).
CC -1- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE
CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR
CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN
CC SHOWN TO BE CALCIUM-SELECTIVE. MAY ALSO BE ACTIVATED BY
CC INTRACELLULAR CALCIUM STORE DEPLETION.
CC -1- SUBUNIT: INTERACTS WITH NHERF (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BRAIN. VERY LOW LEVELS DETECTED
CC IN LIVER KIDNEY, TESTIS, AND UTERUS.
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -1- SIMILARITY: Contains 2 ANK repeats.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, AF029983; AAC13550.1; -
DR EMBL, AF060107; AAF02200.1; -
DR EMBL, AJ006204; CAA06912.1; -
DR MGI, MGI:109524; Trpc5.1;
DR InterPro: IPR002110; ANK.
DR InterPro: IPR002111; Cat_channel_TrpL.
DR InterPro: IPR005821; Ion_trans.
DR InterPro: IPR002153; Trans_receptor.
DR InterPro: IPR004729; Trp_CaChannel.
DR InterPro: IPR005461; TRPChannels.
DR Pfam, PF00023; ANK; 2.
DR Pfam, PF00520; Ion_trans; 1.
DR PRINTS, PRO1097; TRNSRCEPTRP.
DR PRINTS, PRO1646; TRPCHANNELS.
DR SMART, SMO0248; ANK; 2.
DR TIGRFAMs, TIGR00870; trp; 1.
DR PROSITE, PS50088; ANK_REPEAT; FALSE NEG.
DR PROSITE, PS50297; ANK_REPEAT; FALSE NEG.
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW ANK repeat; Repeat; Glycoprotein.
FT DOMAIN 1 330 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 331 351 POTENTIAL.
FT DOMAIN 352 398 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 399 419 POTENTIAL.
FT DOMAIN 420 437 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 438 458 POTENTIAL.
FT DOMAIN 459 470 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 471 491 POTENTIAL.
FT DOMAIN 492 512 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 513 533 POTENTIAL.
FT DOMAIN 534 603 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 604 624 POTENTIAL.
FT DOMAIN 625 975 CYTOPLASMIC (POTENTIAL).
FT REPEAT 69 98 ANK 1.
FT REPEAT 141 170 ANK 2.
FT DOMAIN 630 693 POLY-ARG.
FT SITE 971 973 ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN
FT CARBOHYD 461 461 (BY SIMILARITY).
FT SEQUENCE 975 AA; 111457 MW; DF9248168D3D2D62 CRC64;
SO QUERY MATCH 3.8%; Score 231; DB 1; Length 975;
Best Local Similarity 21.5%; Pred. No. 1.5e-07;
Matches 140; Conservative 98; Mismatches 232; Indels 182; Gaps 28;

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SQ SEQUENCE 981 AA; 112531 MW; 57B172FD65B791C9 CRC64;
 Query Match 3 6%; Score 221; DB 1; Length 981;
 Best Local Similarity 19.6%; Pred. No. 6.9e-07;
 Matches 153; Conservative 105; Mismatches 241; Indels 282; Gaps 31;
 555 LKEMSHLETE--AEARATREAKRYRLALDLFSECSNSEARAF-----ALLVRRNRC 605
 DB 229 LQELSKVENEFSEYBELSRQCK--QFAKDLDDQRRSSELEIILNVRDNL--EEGS 284
 QY 606 WSKTTCGLHATEADAKAFPAHDGVOAFLTRIV-----WGDMAAGTPIRLGLAF 654
 DB 285 GNDLRLKLAIKYRKKEFVAQPNCOOLLASRWYDEFGWRRRHVMVKWTCPIVGL--F 342
 QY 655 LCFALVYNTLIFSEBAPRTGLELDLQDLSLTERKSPYXGQSYBELVEAPRAQGRG 714
 DB 343 PVFSVCY-----LIAPSPV--GL----- 359
 QY 745 PRAVELLTFWRKFGAPVTFGLGVVMPAFLLFTYVLL-----VDRPPPOGSP 765
 DB 360 -----FIKKPFIKFICHTASVLTFL--LLASQHIDRSLNQGPP--PT 402
 QY 766 GPEVTLVFWVFLVLEIRQ--GFTEDETHLVKKFTLYVGDNNKCDMAIFETVGV 822
 DB 403 IYEMWILPWLGLFINGEIKQMDGLQD-----YIDHWNLMDPVMNSLYLATI 451
 QY 823 TCRMLP--SAFE-----AGRTVLMDFVFTLRLIHFAHKOLGPKIIV 866
 DB 452 SKIIVAFVKYSALNPRESWDMHPTLVAEALFALIANISSLRISLFTANSHGLPQLSTL 511
 QY 867 ERMKDVFFFLFELSVMLVAY-----GVTTOAL-LPHDGRLEMTFRVL 910
 DB 512 GMLMDILKFLITVCLVLLAFANGNLQIFYEBETGSCCKGRCKONARSTLF--ETL 570
 QY 911 YRPVLOIFGQPLDEIDARVNCSTHPLLEDSPSCSLYANWLVLLVTLVTLVTL 970
 DB 571 QSLFWSIFGLIN-----LYVTNVKAQHEFTFVGATMGTYNVISLVVL 614
 QY 971 NMLLIAMPSYTPQVQGNATMFKFORVNLIVEYHRPALAP--PELL----- 1017
 DB 615 LMLLIAMMNNSTQLADHADIEKFKRYKLMWSYFEEGGTLPLPPFNVISPKSLMYLW 674
 QY 1018 --SHL-SLTLR-----VFKKEAEH-KREHLERDLPPLDQKV-----TWETVO 1058
 DB 675 IYTHLCKKMKRRKRPESFGITGRADNLRHHQYGVMMNLVRYVAAMIRAKTEBGLT 734
 QY 1059 KENF-----LSQKEK-----RRDSEB----- 1075
 DB 735 EENFKELKODISSFREVELGLRGSXLSTVQSAQGTKESSNSADSEKSDNEGSKDKK 794
 QY 1076 NLSLPLTLTLIHRSAIAAERTTISNGSALVQBPPEKQKRVNVTIRHGLFHRSS 854
 DB 795 NLSLPLTLTLIHRSAIAAERTTISNGSALVQBPPEKQKRVNVTIRHGLFHRSS 854
 QY 1100 KRIKLESQINCVSVSVADVLAQGGPRSSQ-----HCGEGSQVLAADH 1146
 DB 855 KQHAAEQUNANOQFVSSEGAQAQAGPLERSIQLSRTLASRGDLNITGLSQCLVVDH 914
 QY 1147 R 1147
 DB 915 R 915
 RESULT 13
 TRP4 HUMAN STANDARD; PRT; 977 AA.
 AC Q9UBN4; Q15721; Q9UB10; Q9UB11; Q9UB12;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Short transient receptor potential channel 4 (TRPC4) (trp-related protein 4) (http-4) (http4).
 DE TRPC4.
 GN

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 CX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Kidney;
 RX MEDLINE=20498755; PubMed=11042129;
 RA McKay R.R., Szymczek-Seay C.L., Lleyremont J.-P., Bird G.S., Zitt C.,
 RT Juengling E., Lueckhoff A., Putney J.W. Jr.;
 RT "Cloning and expression of the human transient receptor potential 4
 RT (TRP4) gene: localization and functional expression of human TRP4 and
 RL TRP4.";
 RL Biochem. J. 351:735-746(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA; DELTA AND GAMMA).
 RC TISSUE=Embryonic Kidney;
 RX MEDLINE=2109836; PubMed=1163362;
 RA Mery L., Magnino F., Schmidt R., Krause K.-H., Dufour J.-F.;
 RT "Alternative splice variants of htrp4 differentially interact with the
 RT C-terminal portion of the inositol 1,4,5-trisphosphate receptors";
 RL FEBS Lett. 487:377-383(2001).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
 RX MEDLINE=21671347; PubMed=11713258;
 RA Schaefer M., Plant T.D., Streesow N., Albrecht N., Schultz G.;
 RT "Functional differences between TRPC4 splice variants.";
 RL J. Biol. Chem. 277:3752-3759(2002).
 RN [4]
 RP SEQUENCE OF 514-633 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=96234226; PubMed=8646775;
 RA Zhu X., Jiang M., Peyton M., Boulay G., Huret R., Stefani E.,
 RA Birbaumer L.;
 RT "trp, a novel mammalian gene family essential for agonist-activated
 RT capacitative Ca2+ entry.";
 RL Cell 85:661-671(1996).
 CC -1- FUNCTION: THOUGHT TO FORM A RECEPTOR-ACTIVATED NON-SELECTIVE
 CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
 CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR
 CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN
 CC SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY). MAY ALSO BE
 CC ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.
 CC -1- SUBUNIT: Isoform alpha but not isoform beta associates with NHERF
 CC inositol-1,4,5-trisphosphate receptor (trpr). Interacts with NHERF
 CC (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=4;
 CC Name=Alpha;
 CC IsoId=Q9UBN4-1; Sequence=Displayed;
 CC Name=Beta;
 CC IsoId=Q9UBN4-2; Sequence=VSP_006565;
 CC Name=Delta;
 CC IsoId=Q9UBN4-3; Sequence=VSP_006566;
 CC Name=Gamma;
 CC IsoId=Q9UBN4-4; Sequence=VSP_006567; VSP_006569;
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN PLACENTA. EXPRESSED AT
 CC LOWER LEVELS IN HEART, PANCREAS, KIDNEY AND BRAIN. ISOFORM ALPHA
 CC WAS FOUND TO BE THE PREDOMINANT ISOFORM. ISOFORM BETA WAS NOT
 CC FOUND IN PANCREAS AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
 CC SUBFAMILY.
 CC -1- SIMILARITY: Contains 2 ANK repeats.
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DR EMBL; AF063822; AAF22927.1; -
DR EMBL; AF063823; AAF22928.1; -
DR EMBL; AF063824; AAF22929.1; -
DR EMBL; AF063825; AAF22930.1; -
DR EMBL; AF175406; AAD51736.1; -
DR EMBL; AF421358; AAL24549.1; -
DR EMBL; AF421359; AAL24550.1; -
DR EMBL; U40983; AAC50630.1; -
DR GeneW; HGNC:12336; TRPC4.
DR MIM; 603651; -
DR GO; GO:0015279; P:store-operated calcium channel activity; TAS.
DR GO; GO:0006816; P:calcium ion transport; TAS.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat channel_TypL.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR002153; Trans receptor.
DR InterPro; IPR004729; Typ Ca channel.
DR InterPro; IPR005460; TRPChannel4.
DR Pfam; PF00023; ank; 2.
DR Pfam; PF00520; Ion trans; 1.
DR PRINTS; PR01097; TRANSRECEPTP.
DR PRINTS; PR01645; TRPCHANNEL4.
DR SMART; SM00248; ANK; 2.
DR TIGRfam; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_RBP_REGION; 1.
DR Ionic channel; Transmembrane; Ion transport; Calcium channel;
KV ANK repeat; Repeat; Alternative splicing.
FT DOMAIN 1 329 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 330 350 POTENTIAL.
FT TRANSMEM 351 362 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 363 383 POTENTIAL.
FT TRANSMEM 384 436 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 437 457 POTENTIAL.
FT TRANSMEM 458 469 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 470 490 POTENTIAL.
FT TRANSMEM 491 511 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 512 532 POTENTIAL.
FT TRANSMEM 533 599 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 600 620 POTENTIAL.
FT TRANSMEM 621 977 CYTOPLASMIC (POTENTIAL).
FT REPEAT 69 98 ANK 1.
FT REPEAT 141 170 ANK 2.
FT DOMAIN 377 382 POLY-LEU.
FT DOMAIN 615 977 BINDS TO ITPR1, ITPR2 AND ITPR3.
FT SITE 972 974 ESSENTIAL FOR BINDING TO NHERF PDZ DOMAIN (BY SIMILARITY).
FT VARSPLIC 629 693 Missing (in isoform Gamma).
FT VARSPLIC 730 870 Missing (in isoform Delta).
FT VARSPLIC 785 868 Missing (in isoform Beta and isoform Gamma).
SQ SEQUENCE 977 AA; 112100 MM; 77E4D27C37AD660E CRC64;
Query Match 3.6%; Score 219.5; DB 1; Length 977;
Best Local Similarity 19.9%; Pred. No. 8,6e-07;
Matches 156; Conservative 104; Mismatches 235; Indels 289; Gaps 34;

DB 358 -----FIRKPIKICHNASYLTFLFL-----LLASQIHDRSDLNQGP--PT 400
QY 766 GPEVTLYFVWFLVLEIRQ---GFFTEDETHLVKFFLYGDMNNKCDMAIFPIYGV 822
DB 401 IVEWMILFWVAGFTIGELIKOMDGLD-----YHDMNMLDFVNSLYLATI 449
QY 823 TCRMLP---SAFE-----AGRTVLMDFWVFTLRLLIPIAIHKQGPRIIV 866
DB 450 SLKIYAFKYSALNRESMDMMHPTLVAEALFAININISLRLLSLFTANSHLGLOSL 509
QY 867 ERMKDVFETFLFELSVLWVAY-----GYTQAL-LHPDGRLEWIFRRVL 910
DB 510 GRMLDILKFLFIYCLVLLAFANGINQLFYEEETKGLCKGIRCEKONAFSTLF-ETL 568
QY 911 YRPYQIFRGOPLBIDARNCSTHPLLEDSPSCPSLYANWLVILLVFLVLTNVL 970
DB 569 QSLFWSITGLIN-----LYTNVKAQHEFTFEPVATMGTYNVISLVVL 612
QY 971 NMLTIAMPSYTFQVQGNATFMKFORYNLIVEYHERPALAP-PEIL----- 1017
DB 613 LNMILAMNNNSYQLADADLEMKFARFKLMSYFEEGTLPTFPNVIPSPKSLWYLIKW 672
QY 1018 --SHL-SLTLR-----VKKAEH-KREHLERDLPDLDQKV-----TWETVQ 1058
DB 673 IWTHLCKKMKRKPESFGTIGRAADNLRHHQYQEVVRNLVRYVAMIRDAKTEGLT 732
QY 1059 KENF-----LSKMK-----RRDSG----- 1075
DB 733 EENFELKODISSPREFVGLLRGSKLSTIOSANASKSSNSADSDSGSKDKKK 792
QY 1076 -----EVLKRTARVDPIAKYLG-GLREQEK 1100
DB 793 NPSLEDTLLIHPSSAATASERHINISNGSALVQEPPEKQKNFVDIRKFGFHRSS 852
QY 1101 RIKLIESQINCSVLSSVADVLA--QGSGP--RSSQHCSC-----SOLVA 1143
DB 853 KONAENQANQ-----IFSVEVARQQAAGLERNIQLESGLASRGDISIPGLSEQCVL 908
QY 1144 ADHR 1147
DB 909 VDRH 912
RESULT 14
TRP4_MOUSE
ID TRP4_MOUSE STANDARD; PRT; 974 AA.
AC Q9QUQ5; Q62350; Q9QUQ9; Q9QZC0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Short transient receptor potential channel 4 (Trp4) (Receptor-
DE activated cation channel TRP4) (Capacitative calcium entry channel
DE Trp4).
GN TRPC4 OR TRP4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC Tissue=Brain;
RA Zhu X., Boulay G., Jiang M., Birbaumer L.;
RT "Trp4 is involved in capacitative calcium entry in murine cells.";
RL Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.
RN [2]
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RA Qian F., Philipson L.H.;
RL Submitted (Mar-1996) to the EMBL/Genbank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC Tissue=Brain;
RX MEDLINE=98171352; PubMed=9512398;


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OY 911 YRPVIGIQGPPLBIDARVNCSTHPLLEDSPSCPSLYANWVILLVTLVLTAVNL 970
DB 569 QSLFMSIGLIN-----LYTNVQAQHEFEFVATFETYNVLSLVL 612
OY 971 NMLLIAMSTYFQVQVGNATWPKFORYNLIVEYHERPALAP-PELIL----- 1017
DB 613 LNMILIAMNNVSYQIADADADIEKFAKTKLWMSYEEGGTLTPFNVAIPSPKSLMYLVKW 672
OY 1018 --SHL-SLTLRR-----VFKKEAHEKREHLERDLPDLPQKVVTWTVOK--ENFLS 1064
DB 673 IWLHLCKKMRKRPESFGTIGRADNLRHHQ-----YQVWRNLVKRYVA 719
OY 1065 KMEKRRRPSG---EVLAKTARV-DFAKYLIGGREQEKRIKLESQINTCSVLVSSVA 1120
DB 720 AMIREAKTEBGLTENVELKODISSFRFEVLGLRGSKL-----STQSANAASADS 773
OY 1121 DVLAQGGG-----PRSSOHGE-----GSQLVAD 1145
DB 774 DEKQSENGKDKRKNLSLFDLTLIHPRSAIASERHNSLSALVVOE 823

RESULT 15
TRP4_RAT STANDARD: PRT: 977 AA.
AC 035119; Q9EQ74; Q9EQ75;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Short transient receptor potential channel 4 (Trpc4) (Trp4)
DE (Capcative calcium entry channel 1) (CCE1).
CN TRPC4.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC STRAIN=Wistar Imamichi; TISSUE=Brain;
RX MEDLINE=97189270; PubMed=9037541;
RA Funayama M., Goto K., Kondo H.;
RT "Cloning and expression localization of cDNA for rat homolog of TRP
RT protein, a possible store-operated calcium (Ca2+) channel.";
RL Brain Res. Mol. Brain Res. 43:259-266(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC STRAIN=Sprague-Dawley;
RX MEDLINE=20545496; PubMed=10980202;
RA Tang Y., Tang J., Chen Z., Trost C., Flockertzi V., Li M., Ramesh V.,
RA Zhu W.X.;
RT "Association of mammalian trp4 and phospholipase C isozymes with a PDZ
RT domain-containing protein, NHERF.";
RL J. Biol. Chem. 275:37559-37564(2000).
CC -1- FUNCTION: THOUGHT TO FORM NON-SELECTIVE A RECEPTOR-ACTIVATED
CC CALCIUM PERMEANT CATION CHANNEL. PROBABLY IS OPERATED BY A
CC PHOSPHATIDYLINOSITOL SECOND MESSENGER SYSTEM ACTIVATED BY RECEPTOR
CC TYROSINE KINASES OR G-PROTEIN COUPLED RECEPTORS. HAS ALSO BEEN
CC SHOWN TO BE CALCIUM-SELECTIVE (BY SIMILARITY). MAY ALSO BE
CC ACTIVATED BY INTRACELLULAR CALCIUM STORE DEPLETION.
CC -1- SUBUNIT: ISOFORM ALPHA BUT NOT ISOFORM BETA ASSOCIATES WITH
CC INOSITOL-1,4,5-TRIPHOSPHATE RECEPTOR (ITPR). INTERACTS WITH NHERF
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=035119-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=035119-2; Sequence=VSP 006571;
CC -1- SIMILARITY: BELONGS TO THE TRANSIENT RECEPTOR FAMILY. STRPC
CC SUBFAMILY.
CC -1- SIMILARITY: Contains 2 ANK repeats.
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CC -----
DR EMBL; AB008889; BAA23539.1; -
DR EMBL; AF288407; AAC21809.1; -
DR EMBL; AF288408; AAC21810.1; -
DR InterPro; IPR002110; ANK.
DR InterPro; IPR002111; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR002153; Trans_receptor.
DR InterPro; IPR004729; Trp_CaChannel.
DR InterPro; IPR005460; TRPChannel4.
DR Pfam; PF00023; ank; 2.
DR Pfam; PF00520; Ion_trans.1.
DR PRINTS; PRO1097; TRANRECEPTRP.
DR PRINTS; PRO1645; TRPCHANNEL4.
DR SMART; SMO0248; ANK; 2.
DR TIGRfam; TIGR00870; trp; 1.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW Ionic channel; Transmembrane; Ion transport; Calcium channel;
KW ANK repeat; Repeat; Alternative splicing.
FT DOMAIN 1 329
FT TRANSMEM 330 350
FT DOMAIN 351 362
FT TRANSMEM 363 383
FT DOMAIN 384 436
FT TRANSMEM 437 457
FT DOMAIN 458 469
FT TRANSMEM 470 490
FT DOMAIN 491 511
FT TRANSMEM 512 532
FT DOMAIN 533 599
FT TRANSMEM 600 620
FT DOMAIN 621 974
FT REPEAT 69 98
FT REPEAT 141 170
FT DOMAIN 141 170
FT SITE 975 977
FT VAAPSLIC 784 867
FT CONFLICT 11 11
FT CONFLICT 72 76
FT CONFLICT 121 135
FT CONFLICT 204 204
FT CONFLICT 385 411
FT CONFLICT 681 681
FT CONFLICT 705 705
FT CONFLICT 728 728
FT CONFLICT 807 807
FT CONFLICT 873 873
FT CONFLICT 888 888
FT CONFLICT 922 977
SO SEQUENCE 977 AA; 111847 MW; 6F86DA5261E0EDC CRC64;

Query Match 3.5%; Score 216; DB 1; Length 977;
Best Local Similarity 20.2%; Pred. No. 1.5e-06;
Matches 130; Conservative 94; Mismatches 208; Indels 210; Gaps 27;

OY 555 LKEMSHETE--AEAAATREAKTERLALDFSECSNSERAP-----ALLVRNRNC 605
DB 227 LOELSKVNEFKSEYELSRQCK--QFADLDOTRSSRELITILNYRDNDSL--EEOG 282

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QY 606 WSKTCTCHLAHEADAKAFPAHDGVAFLTRW-----WGDMAGSPILRLIGAF 654
Db 283 GNDLARLTKAITYOKEFEVAPORNCQOLASGYDEFGMRRRHVAUKWTCFIIIGL--F 340
QY 655 LCFALVYTNLITFSEEARPLRTGEDLDODLSLDEKSPLYGOSRVELVEAPRAQDRG 714
Db 341 PVFSVCY-----LIAPKSP-L-GL----- 357
QY 715 PRAVFLTRMKKFMGAPVTVLGNVVMYEAFLFTYVLL-----VDFRPPOGFS 765
Db 358 -----FIRKPEIKFICHTASYLTFPL--LLASQHIIDSRLROGP--PT 400
QY 766 GREVTLYFWVTVLVEEIR--GPFEDEDTHLVKKFTLYVGDMNNKCDWALFTIVGV 822
Db 401 IVEWMILPWLVCFTIGELIKOMDGLD-----YHDMNMLDMFVMSLYATI 449
QY 823 TCRMLP--SAFE-----AGRTVLANDFWVTLRLIHFAIHKOLGPKIIV 866
Db 450 SLKIVAFKYSALNPRBSMDMNHPTLVAEALFALINFISSRLISLFPANSHDPLQSL 509
QY 867 ERMKQDFEFLPLFSLWLVAY-----GYTQAL-LHPHDLXMIFFRVY 910
Db 510 GRMLDLIKFLFIYCLVLLAFANGINOLYFYEETKIGSCIGICEKONNAFSTLP-ETL 568
QY 911 YRPVIOFGQIPLDEIDEARVNCSTHPLLEDSPCBSPLVANMVLVLLVAFELVTNVL 970
Db 569 QSLFWSITGLN-----LYTNVKAQHEFTDFGATGFTYVNLISLVL 612
QY 971 NMLLIAMPFSYFOVQGNATFMKFORYNLIVEXHERPALP-PEILSHISLTLRVYK 1029
Db 613 LNMILLAMNNSQOLADHADIDEMKFAKRLKMSYEBEGTLPPTPNV----- 659
QY 1030 KEAHEKHLEHRLDPLDOKVVTWETQ--KENFLSMKEKRRDSEVULRKAHRV-- 1085
Db 660 -----IPSPKS--LMYLVKWIWTHLCKKMKRKEKSEFGTIGRRADNLR 702
QY 1086 -----DFIAKYLGG-LRE-----OEKRICKESQIN 1110
Db 703 HHQIOYMRNLVKRYVAAIMIRAKTEBGLTEBNVELKODIS 744

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Search completed: September 10, 2003, 09:40:14
Job time : 22 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: September 10, 2003, 09:41:20 ; Search time 33 Seconds
(without alignments)
5151.151 Million cell updates/sec

Title: US-09-834-792c-4
Perfect score: 6091
Sequence: 1 MDVQGRPPSPGDAEDRRE.....HRGIDGWEQPGAGQPSDT 1165

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues
Total number of hits satisfying chosen parameters: 541936

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : Published Applications_AA:*
- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/ptodata/2/pubppaa/PCF_NEW_PUB.pep:*
 - 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
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 - 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
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 - 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	6075.5	99.7	1164	9	US-09-834-792-5
2	6073	99.7	1165	14	US-10-026-188-8
3	5068.5	83.2	1158	9	US-09-834-792-2
4	5068.5	83.2	1158	14	US-10-026-188-5
5	4988.5	81.9	1165	14	US-10-026-188-2
6	2430.5	39.9	1214	12	US-10-142-649-2
7	2335	38.3	1083	10	US-09-789-841C-2
8	2041	33.5	1503	12	US-10-153-244-104
9	2041	33.5	1503	14	US-10-210-152-21
10	1578	25.9	1104	12	US-10-171-319-8
11	1578	25.9	1104	12	US-10-171-319-8
12	1562.5	25.7	1095	9	US-09-759-143-778
13	1562.5	25.7	1095	9	US-09-780-669-778
14	1562.5	25.7	1095	9	US-09-822-827-778
15	1562.5	25.7	1095	10	US-09-895-793-778

16	1562.5	25.7	1095	10	US-09-895-814-778	Sequence 778, App
17	1562.5	25.7	1095	12	US-10-144-678A-778	Sequence 778, App
18	1562.5	25.7	1095	14	US-10-012-896-778	Sequence 778, App
19	1562.5	25.7	1095	15	US-10-205-823-421	Sequence 421, App
20	1554.5	25.5	1268	12	US-10-171-319-11	Sequence 11, App1
21	1554.5	25.5	1095	9	US-09-759-143-780	Sequence 780, App
22	1554.5	25.5	1095	9	US-09-780-669-780	Sequence 780, App
23	1554.5	25.5	1095	9	US-09-822-827-780	Sequence 780, App
24	1554.5	25.5	1095	10	US-09-895-793-780	Sequence 780, App
25	1554.5	25.5	1095	10	US-09-895-814-780	Sequence 780, App
26	1554.5	25.5	1095	12	US-10-144-678A-780	Sequence 780, App
27	1554.5	25.5	1095	14	US-10-012-896-780	Sequence 780, App
28	1305.5	21.4	1566	12	US-10-210-152-6	Sequence 6, App1
29	1300.5	21.4	1544	12	US-10-210-152-2	Sequence 2, App1
30	1300.5	21.4	1554	12	US-10-210-152-2	Sequence 2, App1
31	1296.5	21.3	1556	12	US-10-210-152-9	Sequence 9, App1
32	1296.5	21.3	1566	12	US-10-210-152-4	Sequence 4, App1
33	1293	21.2	1579	12	US-10-210-152-10	Sequence 10, App1
34	1228.5	20.2	1533	9	US-09-828-466-7	Sequence 7, App1
35	1228.5	20.2	1533	10	US-09-946-175-1	Sequence 1, App1
36	1228.5	20.2	1533	10	US-09-989-820-259	Sequence 259, App
37	1228.5	20.2	1533	12	US-10-153-244-260	Sequence 260, App
38	1228.5	20.2	1533	12	US-10-210-152-11	Sequence 11, App1
39	1228.5	20.2	1533	15	US-10-281-644-9	Sequence 9, App1
40	1217	20.0	1393	15	US-10-058-513-2	Sequence 2, App1
41	1208.5	19.8	1863	10	US-09-832-292-29	Sequence 29, App1
42	1189.5	19.5	1864	10	US-09-832-292-27	Sequence 27, App1
43	1184	19.4	1970	12	US-10-153-244-4	Sequence 4, App1
44	1183.5	19.4	1864	12	US-10-153-244-6	Sequence 6, App1
45	1180.5	19.4	1939	12	US-10-153-244-6	Sequence 6, App1

ALIGNMENTS

RESULT 1
US-09-834-792-5
; Sequence 5, Application US/09834792
; Patent No. US20020037515A1
; GENERAL INFORMATION:
; APPLICANT: Mount Sinai School of Medicine of NYU
; TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL
; TITLE OF INVENTION: CHANNEL EXPRESSED IN TASTE RECEPTOR CELL
; FILE REFERENCE: AP32911 070165 0589
; CURRENT APPLICATION NUMBER: US/09/834, 792
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,491
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1164
; TYPE: PRT
; ORGANISM: Human
US-09-834-792-5

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Best Local Similarity	99.9%	Pred. No. 0;		
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			Indels	1;
			Gaps	1;
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Qy	61	HLPAFNLVSLVGEQPFPAKSWLRLVLRKGLVLAQSTGAWILTSALRVGLARHVGQAV	120	
Db	61	HLPAFNLVSLVGEQPFPAKSWLRLVLRKGLVLAQSTGAWILTSALRVGLARHVGQAV	120	
Qy	121	RDSHASTSTKRVAVVAVGASLGRVLRRLILEAQEDFPVHYPPDDGSGGCLSDSNL	180	
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Qy	181	SHFLVPPGPKKDDGLTELRLRLERKHSIQRAGVGTGSIETPVLCILVNGDPNTLERI	240	

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Db SRAVEQAAPWMLIVGSGGIADVLALVNQPHLLVPKVAEKQFKFSPSKHFSWEDIVRWT 300
QY KLLONITSHOHLTVYDFEORGSEELDTVILKALVKACKSHSOEPDYLDLKLAVAMDR 360
Db KLLONITSHOHLTVYDFEORGSEELDTVILKALVKACKSHSOEPDYLDLKLAVAMDR 360
QY VDIKSEIFNPDVEMKSCDLEEVWVDALVSNKPEFVRLFVNGADVADFLTYGRLOELYR 420
Db VDIKSEIFNPDVEMKSCDLEEVWVDALVSNKPEFVRLFVNGADVADFLTYGRLOELYR 420
QY SVSRKSLFLDLLQKQEBARLTLAGLGTQARREPPAGPAPSLHVSRLXDFLODACRG 480
Db SVSRKSLFLDLLQKQEBARLTLAGLGTQARREPPAGPAPSLHVSRLXDFLODACRG 480
QY FYODGRPGDRRAEKGPAKRPFGQKWLIDLNQKSNPWRDLFLNAVILQNRHEMATYFWAM 540
Db FYODGRPGDRRAEKGPAKRPFGQKWLIDLNQKSNPWRDLFLNAVILQNRHEMATYFWAM 540
QY GOEGVAAALAAKILIKEMSHLJTEBAARATREAKYERLADLDFSECSNSBARAFALLV 600
Db GOEGVAAALAAKILIKEMSHLJTEBAARATREAKYERLADLDFSECSNSBARAFALLV 600
QY RRNRCSKTTTCHLATEADAKAFPAHDGVOAFLTRIWMGDMAAGTPIRLILGAFICFALV 660
Db RRNRCSKTTTCHLATEADAKAFPAHDGVOAFLTRIWMGDMAAGTPIRLILGAFICFALV 660
QY RRNRCSKTTTCHLATEADAKAFPAHDGVOAFLTRIWMGDMAAGTPIRLILGAFICFALV 659
Db RRNRCSKTTTCHLATEADAKAFPAHDGVOAFLTRIWMGDMAAGTPIRLILGAFICFALV 659
QY YTNLITTFSEEARPLRTGLEDLQDLSDLTDEKSPLYGLOSREBELVAPRAQDGRGRAFL 720
Db YTNLITTFSEEARPLRTGLEDLQDLSDLTDEKSPLYGLOSREBELVAPRAQDGRGRAFL 720
QY LTRMRKFWGAPVTYVLGNVVMYFAFLFTYVLLVDFRPPPGSGPEVTLYFWFTVL 780
Db LTRMRKFWGAPVTYVLGNVVMYFAFLFTYVLLVDFRPPPGSGPEVTLYFWFTVL 780
QY LTRMRKFWGAPVTYVLGNVVMYFAFLFTYVLLVDFRPPPGSGPEVTLYFWFTVL 779
Db LTRMRKFWGAPVTYVLGNVVMYFAFLFTYVLLVDFRPPPGSGPEVTLYFWFTVL 779
QY BEIRGFFTEDEDTLHVKKFTLVYGDNMNKCWMVAFLFLVGVTCMLPSAFBAGRTVLAM 840
Db BEIRGFFTEDEDTLHVKKFTLVYGDNMNKCWMVAFLFLVGVTCMLPSAFBAGRTVLAM 840
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Db BEIRGFFTEDEDTLHVKKFTLVYGDNMNKCWMVAFLFLVGVTCMLPSAFBAGRTVLAM 839
QY DPMVFTLRLIHFALHKQIGPKIIVERMMKDVFFFLPFLSWLVAYGTTQALLHPHDG 900
Db DPMVFTLRLIHFALHKQIGPKIIVERMMKDVFFFLPFLSWLVAYGTTQALLHPHDG 899
QY RLEWIFRRVLYRPLYQIFGOIPLDEIDEARVNCSTHPLLEDSPCSPSLYANMLVILLY 960
Db RLEWIFRRVLYRPLYQIFGOIPLDEIDEARVNCSTHPLLEDSPCSPSLYANMLVILLY 959
QY TELVTVNVLNMLLIAMFSYTFQVVGNAWTFMKFORYNLIVEYHERPALAPFILLSHL 1020
Db TELVTVNVLNMLLIAMFSYTFQVVGNAWTFMKFORYNLIVEYHERPALAPFILLSHL 1019
QY SITLRRVFKKEAHEKHEERLDPDLQKVYTWETVQKENFLSKKEKRRRSEGVLRK 1080
Db SITLRRVFKKEAHEKHEERLDPDLQKVYTWETVQKENFLSKKEKRRRSEGVLRK 1079
QY THARVDFIKYIGGLGEOKRIKLESQINYCSVLSSVADVLAQGGFRSSOHCGESGQ 1140
Db THARVDFIKYIGGLGEOKRIKLESQINYCSVLSSVADVLAQGGFRSSOHCGESGQ 1139
QY LVAADHRGGIDGWEQPGAGQPSDT 1165
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RESULT 2
 US-10-026-188-8
 ; Sequence 8, Application US/10026188
 ; Publication No. US20020164645A1
 ; GENERAL INFORMATION:

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APPLICANT: Zuker, Charles S.
APPLICANT: Zhang, Yifeng
TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
FILE REFERENCE: 02307E-114910US
CURRENT APPLICATION NUMBER: US/10/026,188
PRIOR APPLICATION NUMBER: US 60/259,379
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO: 8
LENGTH: 1165
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human ltrpc6
US-10-026-188-8

Query Match          99.7%; Score 6073; DB 14; Length 1165;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1162; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY HLPAPNLVSLVGEEOPPAPKSWLRDYLRLKLVQAQSTGAWILTSALRVGLAHVQAV 120
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Db HLPAPNLVSLVGEEOPPAPKSWLRDYLRLKLVQAQSTGAWILTSALRVGLAHVQAV 120
QY RDHSLASTSTKVRVVAAGMASLGRVLRHRIIEBAQEDPVHYPPEDDGSQGPLSLDSNL 180
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QY RDHSLASTSTKVRVVAAGMASLGRVLRHRIIEBAQEDPVHYPPEDDGSQGPLSLDSNL 180
Db RDHSLASTSTKVRVVAAGMASLGRVLRHRIIEBAQEDPVHYPPEDDGSQGPLSLDSNL 180
QY SHFLVBERPGKDGDLTELRLERKHSERAGYGTGSIETIVLCLVNGDPNTLERI 240
Db SHFLVBERPGKDGDLTELRLERKHSERAGYGTGSIETIVLCLVNGDPNTLERI 240
QY SRAVEQAAPWMLIVGSGGIADVLALVNQPHLLVPKVAEKQFKFSPSKHFSWEDIVRWT 300
Db SRAVEQAAPWMLIVGSGGIADVLALVNQPHLLVPKVAEKQFKFSPSKHFSWEDIVRWT 300
QY KLLONITSHOHLTVYDFEORGSEELDTVILKALVKACKSHSOEPDYLDLKLAVAMDR 360
Db KLLONITSHOHLTVYDFEORGSEELDTVILKALVKACKSHSOEPDYLDLKLAVAMDR 360
QY VDIKSEIFNPDVEMKSCDLEEVWVDALVSNKPEFVRLFVNGADVADFLTYGRLOELYR 420
Db VDIKSEIFNPDVEMKSCDLEEVWVDALVSNKPEFVRLFVNGADVADFLTYGRLOELYR 420
QY SVSRKSLFLDLLQKQEBARLTLAGLGTQARREPPAGPAPSLHVSRLXDFLODACRG 480
Db SVSRKSLFLDLLQKQEBARLTLAGLGTQARREPPAGPAPSLHVSRLXDFLODACRG 480
QY FYODGRPGDRRAEKGPAKRPFGQKWLIDLNQKSNPWRDLFLNAVILQNRHEMATYFWAM 540
Db FYODGRPGDRRAEKGPAKRPFGQKWLIDLNQKSNPWRDLFLNAVILQNRHEMATYFWAM 540
QY GOEGVAAALAAKILIKEMSHLJTEBAARATREAKYERLADLDFSECSNSBARAFALLV 600
Db GOEGVAAALAAKILIKEMSHLJTEBAARATREAKYERLADLDFSECSNSBARAFALLV 600
QY RRNRCSKTTTCHLATEADAKAFPAHDGVOAFLTRIWMGDMAAGTPIRLILGAFICFALV 660
Db RRNRCSKTTTCHLATEADAKAFPAHDGVOAFLTRIWMGDMAAGTPIRLILGAFICFALV 660
QY YTNLITTFSEEARPLRTGLEDLQDLSDLTDEKSPLYGLOSREBELVAPRAQDGRGRAFL 720
Db YTNLITTFSEEARPLRTGLEDLQDLSDLTDEKSPLYGLOSREBELVAPRAQDGRGRAFL 720
QY LTRMRKFWGAPVTYVLGNVVMYFAFLFTYVLLVDFRPPPGSGPEVTLYFWFTVL 780
Db LTRMRKFWGAPVTYVLGNVVMYFAFLFTYVLLVDFRPPPGSGPEVTLYFWFTVL 780

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Db      721 LTRMKKGAATVFLGNVMTFAFLFTYVLLVDFRPPQSGPGEVTLTFWFTVL 780
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Db      781 BEIRGPFDEBDTHLVKFTLLVYGDNNKCDMAVAFLEFVGTCTMLPSAFEAGRTVLAM 840
Qy      841 DFMVTTLRLLIHFAIHKQIGPKIIVERMKNQVFFPFLFSVWLVAVYVTTQALLHPDG 900
Db      841 DFMVTTLRLLIHFAIHKQIGPKIIVERMKNQVFFPFLFSVWLVAVYVTTQALLHPDG 900
Qy      901 RLEWTFRRVLRVYQIQIIGQIPLEIDEARVNCSTHPLLEDSPSCPSLYANMVLITLLV 960
Db      901 RLEWTFRRVLRVYQIQIIGQIPLEIDEARVNCSTHPLLEDSPSCPSLYANMVLITLLV 960
Qy      961 TELVTVNVLNMLLIAMSYTFQVVOGNATMFKFORVNLIVEYHERPALAPPFILLSHL 1020
Db      961 TELVTVNVLNMLLIAMSYTFQVVOGNATMFKFORVNLIVEYHERPALAPPFILLSHL 1020
Qy      1021 SLLTRRVFKKEAHEKREHLERDLPDLDQKVVTWETVOKENFLSMEXRRRDSGEVLRK 1080
Db      1021 SLLTRRVFKKEAHEKREHLERDLPDLDQKVVTWETVOKENFLSMEXRRRDSGEVLRK 1080
Qy      1081 TAHRTDFIAKYLIGLREDEKRIKLESQINYSVYVSVADVLACGGPSSQHCGBSQ 1140
Db      1081 TAHRTDFIAKYLIGLREDEKRIKLESQINYSVYVSVADVLACGGPSSQHCGBSQ 1140
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Db      1141 LVAADHGGIDGMEQPGAGOPPSDT 1165

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RESULT 3

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US-09-834-792-2
; Sequence 2, Application US/09834792
; Patent No. US20020037515A1
; GENERAL INFORMATION:
; APPLICATION: Mount Sinai School of Medicine of NYU
; TITLE OF INVENTION: TRP8, A TRANSIENT RECEPTOR POTENTIAL
; FILE REFERENCE: CHANNEL EXPRESSED IN TASTE RECEPTOR CELL
; CURRENT APPLICATION NUMBER: US/09/834,792
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,491
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Murine TRP8
US-09-834-792-2

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Query Match      83.2%; Score 5068.5; DB 9; Length 1158;
Best Local Similarity 83.9%; Pred. No. 0;
Matches 980; Conservative 66; Mismatches 109; Indels 13; Gaps 4;

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Db      1 MOTTSSCPGSPPTDEGMEPLTCRGEINFGSGKKRKFVPSVAPSVLFEILLTEW 60
Qy      61 HLPAPNLVSVLGEORPFAKSMWLDVLRKGLVKAOSTGAMIIILSALRVGLARHVGAV 120
Db      61 HLPAPNLVSVLGEORPFAKSMWLDVLRKGLVKAOSTGAMIIILSALRVGLARHVGAV 120
Qy      121 RDHSLASTSTKRVVAVAGMASIGRVLRRIIE--EAQEDFVHVYEDDGSQGPICLSDS 178
Db      121 RDHSLASTSTKRVVAVAGMASIGRVLRRIIE--EAQEDFVHVYEDDGSQGPICLSDS 178
Qy      179 NLSHFLLVPEPPGPKG-DGLTELRLRLKHTSEQAGVGGGSLIEPVLCLLVNDPDTL 237
Db      179 NLSHFLLVPEPPGPKG-DGLTELRLRLKHTSEQAGVGGGSLIEPVLCLLVNDPDTL 237
Qy      181 NLSHFLVSGALSGGNDGLTELQSLSEKHSQQRTGIGTSCIOIPVLCLLVNDPDTL 240
Db      181 NLSHFLVSGALSGGNDGLTELQSLSEKHSQQRTGIGTSCIOIPVLCLLVNDPDTL 240

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Qy      238 ERISRAVEQAAPMLILVSGGSIADVLALVNQPHLVPKVAEQFKEXPSKHSWEDIV 297
Db      241 ERISRAVEQAAPMLILVSGGSIADVLALVNQPHLVPKVAEQFKEXPSKHSWEDIV 300
Qy      298 RMTKLQNTSHTQHLTYYPDEGSEELDVIIKALVKACKSHSOEPODVLDELKALA 357
Db      301 HMTLQNTSHTQHLTYYPDEGSEELDVIIKALVKACKSHSOEPODVLDELKALA 360
Qy      358 WDRVDAKSEIFNGDVEKSCDLEENWADALVSNKPEFVRFLVYNGADVADFLTYGRLOE 417
Db      361 WDRVDAKSEIFNGDVEKSCDLEENWADALVSNKPEFVRFLVYNGADVADFLTYGRLOE 420
Qy      418 LYSVSRSKSLIFDLQKQSEARLLTAGLGTQARPEPPAGPAPSLHEVSRVLKDFLODA 477
Db      421 LYSVSRSKSLIFDLQKQSEARLLTAGLGTQARPEPPAGPAPSLHEVSRVLKDFLODA 480
Qy      478 CRGFYQDGRPEDDRRAEGRPKRPTGQKWLIDLQKSENPFRDLFLNAVLQNRBMATYF 537
Db      481 CRGFYQDGRPEDDRRAEGRPKRPTGQKWLIDLQKSENPFRDLFLNAVLQNRBMATYF 536
Qy      538 WAMQEGVAAALAAKILKEMSHLETEAARATREAKYERLALDLFSECVSNSEARAF 597
Db      537 WAMQEGVAAALAAKILKEMSHLETEAARATREAKYERLALDLFSECVSNSEARAF 596
Qy      598 LIVERNRQWSTKTLHATEADAKAFPAHGVQAFLTRIMWGDMAAGTPILRLGAFICP 657
Db      597 LIVERNRQWSTKTLHATEADAKAFPAHGVQAFLTRIMWGDMAAGTPILRLGAFICP 656
Qy      658 ALVYTNLTTSBEAPLRTGLEDDLDLSDTEKSPLYGLOSREVELYEPAPQDGRPRA 717
Db      657 ALVYTNLTTSBEAPLRTGLEDDLDLSDTEKSPLYGLOSREVELYEPAPQDGRPRA 716
Qy      718 VELLTRMRKFWGAVTVFLGNVMTFAFLFTYVLLVDFRPPQSGPGEVTLTFWFTVL 777
Db      717 AFLTRMRKFWGAVTVFLGNVMTFAFLFTYVLLVDFRPPQSGPGEVTLTFWFTVL 776
Qy      778 LVLEIRIQGFTEBDTHLVKFTLLVYGDNNKCDMAVAFLEFVGTCTMLPSAFEAGRTV 837
Db      777 LVLEIRIQGFTEBDTHLVKFTLLVYGDNNKCDMAVAFLEFVGTCTMLPSAFEAGRTV 836
Qy      838 LAMPFWFTLRLLIHFAIHKQIGPKIIVERMKNQVFFPFLFSVWLVAVYVTTQALLHP 897
Db      837 LAMPFWFTLRLLIHFAIHKQIGPKIIVERMKNQVFFPFLFSVWLVAVYVTTQALLHP 896
Qy      898 HDGRLEWIFRRVLKRPYLQIFGOIPLEIDEARVNCSTHPLLEDSPSCPSLYANMVLIT 957
Db      897 HDGRLEWIFRRVLKRPYLQIFGOIPLEIDEARVNCSTHPLLEDSPSCPSLYANMVLIT 956
Qy      958 LVTFLTVTNVLNMLLIAMSYTFQVVOGNATMFKFORVNLIVEYHERPALAPPFILLS 1017
Db      957 LVTFLTVTNVLNMLLIAMSYTFQVVOGNATMFKFORVNLIVEYHERPALAPPFILLS 1016
Qy      1018 SHLSLTLRRVFKKEAHEKREHLERDLPDLDQKVVTWETVOKENFLSMEXRRRDSGEV 1077
Db      1017 SHLSLTLRRVFKKEAHEKREHLERDLPDLDQKVVTWETVOKENFLSMEXRRRDSGEV 1076
Qy      1077 LRKTAHRVDPLAKYLIGLREDEKRIKLESQINYSVYVSVADVLACGGPSSQHCGBSQ 1137
Db      1077 LRKTAHRVDPLAKYLIGLREDEKRIKLESQINYSVYVSVADVLACGGPSSQHCGBSQ 1136
Qy      1138 GSQLVADHGGIDGMEQPGAGOPPSDT 1165
Db      1137 RSQPAASAR-----EYLSGGLPPSDT 1158

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RESULT 4

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US-10-026-188-5
; Sequence 5, Application US/10026188
; Publication No. US20020164645A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California

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; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
; TITLE OF INVENTION: Ion Channel
; FILE REFERENCE: 02307E-114910US
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/259,379
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 5
; LENGTH: 1158
; TYPE: prt
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: mouse ltrpc5 predicted amino acid sequence
; US-10-026-188-5

Query Match      83.2%; Score 5068.5; DB 14; Length 1158;
Best Local Similarity 83.9%; Pred. No. 0;
Matches 980; Conservative 66; Mismatches 109; Indels 13; Gaps 4;

QY 1 MODVGPSPGPDADREELGLHGEVNFSGSKKRGKFRVPSGAPSVLPDLLAEW 60
DB 1 MOTTSSCPSPPTEDGWEPIICRGEINFGSGSKKRGKFRVPSVAPSVLPFELLTEW 60
QY 61 HLPAPNLVSVLGEQPFAMKSMRLDVLRKGLVKAOSTGAMILTSALHVGARHVGAV 120
DB 61 HLPAPNLVSVLGEQPFAMKSMRLDVLRKGLVKAOSTGAMILTSALHVGARHVGAV 120
QY 121 RDHSLASTSTKRVAVAVAGASLGRVLRHRIE--EAQEDPVPVHPEDDGSOGPLCSLDS 178
DB 121 RDHSLASTSTKRVAVAVAGASLGRVLRHRIE--EAQEDPVPVHPEDDGSOGPLCSLDS 180
QY 179 NLSHFLIVEPSPGKG-DGLTELRLLEKHISEQRAQYGTGSIIEIPVLCILVNGDPNTL 237
DB 181 NLSHFLIVEPSPGKG-DGLTELRLLEKHISEQRAQYGTGSIIEIPVLCILVNGDPNTL 240
QY 238 ERISRAVEQAPMLILVSGSGIADVLAALVNGPHILVPAVKQPEKPEKPSSECFSEALIV 297
DB 241 ERISRAVEQAPMLILVSGSGIADVLAALVNGPHILVPAVKQPEKPEKPSSECFSEALIV 300
QY 298 RMTKLQNTTSHQHLTVDFEQQSGSEEDTVILKALVACKSHSQPODYLDELKLAVA 357
DB 301 HMTLQNTTSHQHLTVDFEQQSGSEEDTVILKALVACKSHSQPODYLDELKLAVA 360
QY 358 MDRVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKEPVRLLPYDNGADVADPILTGRLQ 417
DB 361 MDRVDIAKSEIFNGDVEMKSCDLEEVMDALVSNKEPVRLLPYDNGADVADPILTGRLQ 420
QY 418 LVRSVSRKSLFDLLQKQEBARLTLAGICTQOAREPPAPRAFSLHEVSRVLKDFLOPA 477
DB 421 LVRSVSRKSLFDLLQKQEBARLTLAGICTQOAREPPAPRAFSLHEVSRVLKDFLOPA 480
QY 478 CRGFYODGRPGDRRAEKSPAKRPTGQKWLDDLQKSEPMWDLFLMAVLQNRHEMATYF 537
DB 481 CRGFYODG---RRMERGPSPKRPAGQKLPDLRSKSEDPMDLFLMAVLQNRHEMATYF 536
QY 538 WAMGQGVAAALAAKCIKEMSHLETEAARATREAKYERLALDLPSCYCSNSEARAPA 597
DB 537 WAMGREGVAAALAAKCIKEMSHLEKEAEVARTREAKYEQIALDLFSECYCSNSEARAPA 596
QY 598 LVRRRRCSTKTCCLHATEADAKAFPAHDGVOAFLTRIWMGMAGTPIRLILGLFLOF 657
DB 597 LVRRRHSWSRTTCHLATEADAKAFPAHDGVOAFLTKIWMGMAGTPIRLILGLFLOF 656
QY 658 ALVYTNLITFSEBAPRTGLIEDLQDSDLTESKPYGLQSRVEELVEAPRAQDGRPA 717
DB 657 ALVYTNLITFSEBAPRTGLIEDLQDSDLTESKPYGLQSRVEELVEAPRAQDGRPA 716
QY 718 VPLLTWRKFWGAPVTVFLGNVVMYPAFLPLFTYVLLVDFPRPQSPGSEVTLTYWVFT 777
DB 717 AFLLTWRKFWGAPVTVFLGNVVMYPAFLPLFTYVLLVDFPRPQSPGSEVTLTYWVFT 776

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QY 778 LVLEIRQGFTEDEDTLHVKKFTLYVGNMNMCDMVAIFLEIVGTCMLSPAREAGRTV 837
DB 777 LVLEIRQGFTEDEDTLHVKKFTLYVEDNMNMCDMVAIFLEIVGTCMVSFBAGRTV 836
QY 838 LAMPWVFTLLIHIFAIHKQLGKIIYVERMKDVFVFLFSLVWLVAYGVTTQALLHP 897
DB 837 LAIDFMVFTLLIHIFAIHKQLGKIIYVERMKDVFVFLFSLVWLVAYGVTTQALLHP 896
QY 898 HDGRLEWIFRRVLRPVYQIFGOIPLDEIDBARVNCSTHPLLEDSPSCPSLYANMLVIL 957
DB 897 HDGRLEWIFRRVLRPVYQIFGOIPLDEIDBARVNCSTHPLLEDSPSCPSLYANMLVIL 956
QY 958 LVLFTLVTVNLVNLMLIAMESYTFQVVGNAFMFKFORVNLIVEYHERPALAPFTLL 1017
DB 957 LVLFTLVTVNLVNLMLIAMESYTFQVVGNAFMFKFORVNLIVEYHERPALAPFTLL 1016
QY 1018 SHLSITLRRVRKGAHEKHEHLERDLPPLDQKVVYTWTVQKENTLSMEKRRRSEGEV 1077
DB 1017 SHLSITLRRVRKGAHEKHEHLERDLPPLDQKVVYTWTVQKENTLSMEKRRRSEGEV 1076
QY 1078 LRKTAHRVDLAKYIGLRBQEKRIKLESQIYCSVLVSSVADVLAQGGPRSSQHCGE 1137
DB 1077 LRKTAHRVDLAKYIGLRBQEKRIKLESQIYCSVLVSSVADVLAQGGPRSSQHCGE 1136
QY 1138 GSQLVADHRGIDGMEQPGAGOPPSDT 1165
DB 1137 RSQPASARD-----EYLESGLPPSDT 1158

RESULT 5
US-10-026-188-2
; Sequence 2, Application US/10026188
; Publication No. US20020164645A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Zhang, Yifeng
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Assays for Taste Receptor Cell Specific
; TITLE OF INVENTION: Ion Channel
; FILE REFERENCE: 02307E-114910US
; CURRENT APPLICATION NUMBER: US/10/026,188
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/259,379
; PRIOR FILING DATE: 2000-12-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 1165
; TYPE: prt
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat L-TRP taste predicted protein
; US-10-026-188-2

Query Match      81.9%; Score 4988.5; DB 14; Length 1165;
Best Local Similarity 82.6%; Pred. No. 0;
Matches 963; Conservative 76; Mismatches 116; Indels 11; Gaps 3;

QY 1 MODVGPSPGPDADREELGLHGEVNFSGSKKRGKFRVPSGAPSVLPDLLAEW 60
DB 9 MEMAOSGCPSPPTEDGWEPIICRGEINFGSGSKKRGKFRVPSVAPSVLPFELLTEW 68
QY 61 HLPAPNLVSVLGEQPFAMKSMRLDVLRKGLVKAOSTGAMILTSALHVGARHVGAV 120
DB 69 HLPAPNLVSVLGEQPFAMKSMRLDVLRKGLVKAOSTGAMILTSALHVGARHVGAV 128
QY 121 RDHSLASTSTKRVAVAVAGASLGRVLRHRIE--EAQEDPVPVHPEDDGSOGPLCSLDSNL 180
DB 123 RDHSLASTSTKRVAVAVAGASLGRVLRHRIE--EAQEDPVPVHPEDDGSOGPLCSLDSNL 188
QY 181 SHFLIVEPSPGKG-DGLTELRLLEKHISEQRAQYGTGSIIEIPVLCILVNGDPNTLER 239
DB 189 SHFLIVEPSPGKG-DGLTELRLLEKHISEQRAQYGTGSIIEIPVLCILVNGDPNTLER 248

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QY	240	SRBAVEOAAPMLIIYVGGSGIADVAVLALVNQPHLLVLPKVAEKQPKKEPSEKSHSWEDIVRW	299
Db	249	MSRAVEOAAPMLIIYVGGSGIADVAVLALVQPHLLVPQVTEKQPKREFPSECECSWEIVRW	308
QY	300	TKLQONISHQHLITVYDFEAGESEELDVIIKALVAKACKSHOSEPODYLDLKLAVAMD	359
Db	309	TELLQNIAMHPLHLYTVDFEAGESEELDVIIKALVAKACKSHSRADQYLDLKLAVAMD	368
QY	360	RVDIAKSEIFNGDVEMKSCDLEEVNVDALVSNKPEVRLFVJNGADVADFLTYGRLOELY	419
Db	369	RVDIAKSEIFNGDVEMKSCDLEEVNVTDALVSNKPDFVRLFVJNGADMAEFLTYGRLOELY	428
QY	420	RSVSKSLIFDLQKQOEABRLTLAGLGTQQAAREPPAGPAPASLHEVSVLKDPLQDACR	479
Db	429	HSVSKSLIFELLERKHEBGRLLTLGLQOQTRKPLVPGAPASLHEVSVLKDPLHDAQR	488
QY	480	GFYQDGRPDQRRRAEKGPAPRPTGQKMLDLNQSXENPMRDLFPLVAVLQNRHEMATYFWA	539
Db	489	GFYQDQ-----RMEKRGKPPKRPAGQKMLPDLRSKSEDPMRDLFPLVAVLQNRHEMATYFWA	544
QY	540	MGQSEVAAAALAACTLLKEMSHLETPAARATREAKYERLALDLPSECTYSNSBARAFLL	599
Db	545	MGREVAAAALAACTIIKEMSHLEKAEAVARTREAKYEQALADLPSECTYSNSBARAFALL	604
QY	600	VRRNCSWKTCTGLHATEADAAFAFHQGVQAFRLRIMWGDMAACTPILRLGATLCPAL	659
Db	605	VRRNCSWRTTCLHATEADAAFAFHQDVQAFRLKIMWGDMACTPILRLGATTCPAL	664
QY	660	VYTNLIITSEEARPLRTGLEDLQDLPLDTEKSPGLYGOSRVELEAPRAQGRDRAFAF	719
Db	665	IYTNLIISSEDAPOQMDLEDLQEPDLSDMKXSFLOSHGQLEKLEAPRAPDLDGQAAF	724
QY	720	LLTRRRKRWGAPVTVFLGNVWVYFAPFLFTYVLLVDRPRPQSGSGREVTLYFVNFVTLV	779
Db	725	LLTRRRKRWGAPVTVFLGNVWVYFAPFLFTSVLLVDRPRPQSGSGSEVTLYFVNFVTLV	784
QY	780	LEEIQGFETDEDTHLYKKFTLYVGDNNKCDMAVILFLTVGTCRMLPSAEAGRTVLA	839
Db	785	LEEIQGFETDEDTHLYKKFTLYVEDNNKCDMAVILFLTVGTCRMPVSFEAGRTVLA	844
QY	840	MDFWFTLRLIHIFAIHQGLGPKIIIVERMKDVFFFLFSLVSVLVAAGVTTQALLHPHD	899
Db	845	IDFWFTLRLIHIFAIHQGLGPKIIIVERMKDVFFFLFSLVSVLVAAGVTTQALLDHPD	904
QY	900	GRLEWIFRRVLYRPVLOIFGQIPLDEIDBARVNGSTHPLLEDSPSCSLYANMLVILLL	959
Db	905	GRLEWIFRRVLYRPVLOIFGQIPLDEIDBARVNCSLHPLLEDSSASCPLLYANMLVILLL	964
QY	960	VTFLLVTVNVLNMLLIAMFSYTFQVQONATYEMKFORVNIIVEHBRPALAPRILLISH	1014
Db	965	VTFLLVTVNVLNMLLIAMFSYTFQVQONADFMFAKORHLILVEYHGRPALAPRILLISH	1022
QY	1020	LSLTLRVYFKKAEKREHLEHDLDPDLDQKVTVETVQKCNFLSKMEKRRRDSGEVYLR	1079
Db	1025	LSLTLVYKFRKBAHQHQLERHDLDPDQKIIITVETVQKCNFLSTWMEKRRRDSKEVYLR	1084
QY	1080	KTARHVDVIAKYLGLRQEKRIKCLBEOQINCSVLVSSVADVLAQGGSPRSSQHCGBGS	1133
Db	1085	KTARHVDVIAKYLGLRQEKRIKCLBEOQANCMLLSSMTDTLAPGGTYSSQNCGRSS	1144
QY	1140	QLVADHRCGIDGMEQPGAGOPSPDT	1165
Db	1145	QPASARDR-----EYLEAGLPHSDT	1164

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; FILE REFERENCE: A-71325-2/RFT/NBC
; CURRENT APPLICATION NUMBER: US/10/142,649
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: 60/351,938
; PRIOR FILING DATE: 2002-01-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 1214
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-142-649-2

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Query Match	39.9%	Score 2430.5	DB 12	Length 1214
Best Local Similarity	45.4%	Pred. No. 3.9e-216		
Matches	532	Conservative 177	Mismatches 352	Indels 111
Qy	26	GEVNFPGSGKKRGRFVRVSGVAPSVLFDLLAEWHLPAPNIVSLVSGEOPFAMKSWIR	85	
Dy	76	GELDFPTGAGRGKSHNFLRISDRTPDAVAVSVLVRTRTGFPAPNIVSVLGGSGGVPQTWIIQ	135	
Qy	86	DVLKKGIVKVAOSNGAMVLTSLANRGLARHNGQARHDSLASTKTRVRVAAGMALGRV	145	
Dy	136	DLKRGVLRAAOSTGAMVLTGGLHGTGRHGVAVRADHOMASTG-GTKVAANGVAWGVV	194	
Qy	146	LHRRILIEAEDFPVHY-?-PEDDGSQGPLCLSDNLSHFILVEPFPKGDELTEL	200	
Dy	195	RNRDTLNPKSPFARYWRQDPED-GVQRP--LDVYNASFVLDDSTHCLGSENF	249	
Qy	201	RLRLKHISEORAGYGTGSTIEIPVCLLVNGDPNTLERISAVBOAWMLVLSGSGIA	260	
Dy	250	RLRLSEYSIOOKTGVGGTG-IDIPVLLILIDGDEKMLTRIENATOAQPLCLLVAGSGAA	308	
Qy	261	DVLALVNOQPLVLP-----KVAEKOFKEKFPKSHSWENIVMTYKLQNTSHQHL	313	
Dy	309	DCLAEITLED--TLAPGSGARQGEARDRIRRFPR- -GDVLVQAQVEIMTRKELL	361	
Qy	314	TVYDFEOGSEELDTVILKALVKAKSHSOEPODYLDKLKLVANDRVDIAKSEIFNGV	373	
Dy	362	TVYSE--DGSEEFETIVKALVKK--CSSEASAVLDELRLAVANNRVDIQSELFRGDI	418	
Qy	374	EMKSCDLEEVNVADLVNSKPEFVNLFVUNGADVDFLYYGRLOELYRSVRSKSLFLDLQ	433	
Dy	419	QMRSPHLSEASLMDALLNDPRFVLLISHGSLGHFLTPMRADQYSAAPSNSLIRNLLD	478	
Qy	434	RKQEARLTLAGL--GTQOAREPPAPGPAFLHEYSRVLKPLOACRQFYODGRGDR	491	
Dy	479	QASHSAGTKAPALKGAAELRPP-----DVGHVLRMLLGKMCARVYSGGAWDH	528	
Qy	492	RAEKGPAPKPTGQKMLDLNOKS-----ENFWRDLFWAVLQNRHEMATYFWAMQ	542	
Dy	529	-----PGGFEESWYLLSDKATSPISLDAGLGQAPWSDLLMALLINRQAMQMYEWEMGS	583	
Qy	543	EGVAAALAAACKILKEMSHLETAEAEAAARTRE--KYETLADLPSECYNSNSAPAFALV	600	
Dy	584	NAVSASAGACLLLVMARLEPDAEBAARKDLAFKEFGMGVDLPSECRSSSVRAARLL	643	
Qy	601	RNRNCSKTTCLHATEADAKAPFAHGVQVAFLTRIMWGDMAAGTPILRLGLAFLCFALV	660	
Dy	644	RRCPLMDATCLOAMQADARAPFAODGVSLTLQKMWGDMASTPIWALVLAFCPLI	703	
Qy	661	YTNLITF--SPEALVRGLDELQDLSDLTREKSPLYGQSVSEELVEAPRAQD-----	712	
Dy	704	YTRILTRKEEETRELE--FMDSVINGEGPVTADPAEKPTLGVPRSGRQCCGG	761	
Qy	713	--RRPRAVFLTRRRKFWGAPVTVFLGVNWWYFAFLFTVVLVDFPRPPGSGPEVT	770	
Dy	762	RCGRRRC--LRRFHFHWGAPVTIFMGVNVSYLFLFLPSKVLVDFQAP--PESLELL	816	
Qy	771	LYFVVFVLVLEIRIQGFPTDEDT-----HLVKKFTLVYGDNNKCDMAVFLFI	819	
Dy	817	LYFVAFLTLCEELIQGLSGGGSJLASGGPGGHASLQRLRLVLYADSNQCDLVALLTCL	876	

QY 820 VGVTCRMLPSAEAGRTVLANDFMVFTLRLHI PAIHKOLGPKTIIVERMMKDVFFPLFF 879
 DB 877 LGVGRRLTFLGLHGRYUCLIDFMVFTYRLHI FTVNNQLGPKIYIVSGMMKDVFFPLFF 936
 QY 880 LSVMLVAAGVTTQALLHPHGRLEMI FRRVLYRPLYQIFGQIPLEIDEARV--NCSTH 936
 DB 937 LGVMLVAAGVATEGLLRPRSDPFI LRVRVFRPLYQIFGQIPQEDMDVALMEHNSCSE 996
 QY 937 PULLEDSP-----SCPSLYANMLVLLVLTPLJNNVLLMMLIMFSTFQVGNATM 991
 DB 997 PGMWHPGQAQAGTCVSOQYANMLVLLVLTPLJNNVLLMMLIMFSTFQVGNATM 1056
 QY 992 FKKFORVNLIVEYHRPALAPFILLSHLSTLRVFKK-----EAEHREHLEBD 1042
 DB 1057 YWKARVRLIRFHRPALAPFIFYI SHRLRLRQLCRRPRSPQSSPALHFRVYLSKE 1116
 QY 1043 LPDPLDQVVTWEVOKENFLSKMEKRRRDSGEVLAKTAHVDPIAKYLGRLRQEKTI 1102
 DB 1117 ---AERKLTWESYHKNFLLARADKRESDESERLKRTSQKVDLALKQIGHIREYQRL 1172
 QY 1103 KCLSEQINVCVLSVSSVADVLAQ-----GCP 1129
 DB 1173 KVLEREVOQCSRVLGWVMAELSRALLPFGP 1204

RESULT 7

US-09-789-481C-2
 ; Sequence 2, Application US/09789481C
 ; Patent No. US20020142377A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Glucksmann, Maria Alexandra
 ; APPLICANT: Curtis, Rory A.J.
 ; APPLICANT: Lora, Jose M.
 ; TITLE OF INVENTION: 18607, A No. US20020142377A1 Human Calcium Channel
 ; FILE REFERENCE: MNI-097CP3
 ; CURRENT APPLICATION NUMBER: US/09/789,481C
 ; CURRENT FILING DATE: 2001-02-20
 ; PRIOR APPLICATION NUMBER: 09/510,706
 ; PRIOR FILING DATE: 2000-02-22
 ; PRIOR APPLICATION NUMBER: 09/634,669
 ; PRIOR FILING DATE: 2000-08-08
 ; PRIOR APPLICATION NUMBER: 09/583,373
 ; PRIOR FILING DATE: 2000-05-31
 ; NUMBER OF SEQ ID NOS: 3
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 1083
 ; TYPE: PRP
 ; ORGANISM: Homo sapiens
 US-09-789-481C-2

Query Match 38.3%; Score 2335; DB 10; Length 1083;
 Best Local Similarity 45.7%; Pred. No. 2.5e-207;
 Matches 513; Conservative 165; Mismatches 338; Indels 106; Gaps 25;
 QY 39 KTVRVSSGAPSVLPDLLAEMLPAPNIVSLVGEQPRAMKSWLRDVLKGLVYAAOS 98
 DB 4 QFRLSDRDPDAVSVLVRTRWGFRAPNLVSVLGGSGGVLTQWLDLRLKGLVYAAOS 63
 QY 99 TGMILTSALRVGLARHVAQAVDHSLASTSTKRVVAVAGMASLGRVLRRLIEAODEP 158
 DB 64 TGMITITGGLHIGIHGVAADHOMASNG-CTKVAVAGVAVRWRRDITLJNKGSF 122
 QY 159 PWHY-----PEDDGSQGPLCSIDSNLSHFILVEPGRPGKDGTLRLRLEKHISEORA 213
 DB 123 PARVWRGDPED--GVQFP---LDVYVSAFFLVDDTHGCLGSENFRLRLIESYISQOKT 177
 QY 214 GVGCTGSIHPVLCILVNDPNTLERISAVEQAAMVLLVGGGTAADVLAALVNGPHL 273
 DB 178 GVGCTG-IDIVLLLLIDGEEKLTRIENATQALPCLLVAGSGGAADCAETLED--TL 234
 QY 274 VP-----KVAEKQPKPKPSKGFMSMEDIVRWTKLLQNTTSQHLLTVVDFQESSEET 326

DB 215 APGSGAGQGEARDRIRRFPPK-----GDLEVLQAQVERIMTRKELLTVYSSE-DGSEEF 288
 QY 327 DTVLKALVYKCKSHSQSPODYDELKLAVAMDRVDAKSEIFNGDVEMKSCDLEBVMVD 386
 DB 289 ETIVKALVYKCK--GSSBASAYLDELRLAVAMNRVDIASELFRDIDWRSHLEASLMD 346
 QY 387 ALVSNKPEFVRLFVDNGADVADFLTYGRLQELLYRSVSKSLFDDLQKQEBARLTLAGL 446
 DB 347 ALLNDRPEFVRLLSHGSLGHLFTPMRLAQYSAAPNSILRLNLLDQASHAGTKAPAL 406
 QY 447 --GTQAAEPAPGAPPAFSLHEYSRLKDFLQDAGCGFTQDGRPGGRRAEKAPRPTQ 504
 DB 407 KGAAGELRPP-----DVGHVLRMLGCMCAPRYPGGAWPH-----PGGPGES 451
 QY 505 KMLDLNQS-----ENPMRDLFLMAVLQONHEMATYFAMAGQEVAAALAAKIL 555
 DB 452 MYLLSDKATSPSLDAGLGQAPVMSLLMLALLNRAQMAAMTFMENGSAVASALACILL 511
 QY 556 KEMSHLETEAEARATREA--KYERIALDLFSECYSNSBARAFALLVRNRCSKTTCLH 613
 DB 512 RVMARLEPDAEBAARXOLAFKFEQMGVDLFGECYRSEVRARLLRRCPIMGDATCLQ 571
 QY 614 LATEADAAQFPAHQVQAFRLTRIMWGDMAAGTPIRLGAFICFALVTNLTTF--SEEA 671
 DB 572 LAMQADARAFPAQDVGOSILTOXWGDMASTPIWALVAFPCPLIYTRLITFRKSEBE 631
 QY 672 PLRTGLELDLSDLTDEKSPLYGLQSRVEELVEAPRAQD-----RGPRAVFLTR 723
 DB 632 PTREBLE--FMDSDVINGEPVGTADPAEKPLPGVPROSGRGCCGCGGRC--LRR 686
 QY 724 WRKFGAPVTVFGLGVNVMYFAFLFLTYVLLVDFRPPPGSGSPRETVLYFVFTLVLEI 783
 DB 687 WFFHWGAPVTIFMGVNVSTLFLFLFSRLVLDVFPAP--PESLELLYFMAFTLLCEBL 744
 QY 784 ROGFTEDEDT-----HLVKKFTLYGDDNNKCDMAVIFLPIYGVTCRMLPSAE 832
 DB 745 ROGLSGGGGSLASGPGRGHSLSORLRLYLDSSMNCODLVALTFFLGVGRLTPGLVH 804
 QY 833 AGRTVLANDFMVFTLRLHI PAIHKOLGPKTIIVERMMKDVFFPLFSLVMLVAVGTTQ 892
 DB 805 LRTVLCIDFMVFTYRLHI FTVNNQLGPKIYIVSGMMKDVFFPLFGLVMLVAVGATE 864
 QY 893 ALLHPHGRLEMI FRRVLYRPLYQIFGQIPLEIDEARV--NCSTHPLLEDSP----- 944
 DB 865 GLLRPRDPSPI LRVRVFRPLYQIFGQIPQEDMDVALMEHNSCSEPFMAHPGQAQ 924
 QY 945 SCPSLYANMLVLLVLTPLJNNVLLMMLIMFSTFQVGNATMFKFORVNLIVEY 1004
 DB 925 TCVSQYANMLVLLVLTPLJNNVLLMMLIMFSTFQVGNATMFKFORVNLIVEY 984
 QY 1005 HERPALAPFILLSHLSTLRVFKK-----EAEHREHLEBDLPDQKVVTWE 1055
 DB 985 HSRPALAPFIFYI SHRLRLRQLCRRPRSPQSSPALHFRVYLSKE---AERKLTWE 1040
 QY 1056 TVQKENFLSKMEKRRRDSGEVLAKTAHVDPIAKYLGRLRQEKTI 1097
 DB 1041 SVHKNFLLARADKRESDESERLKRTSQKVDLALKQIGHIRE 1082

RESULT 8

US-10-153-244-104
 ; Sequence 104, Application US/10153244
 ; Publication No. US20030144191A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER, TRP-2L
 ; TITLE OF INVENTION: SPLICE VARIANTS THEREOF
 ; FILE REFERENCE: D0144 NP
 ; CURRENT APPLICATION NUMBER: US/10/153,244
 ; CURRENT FILING DATE: 2002-05-22
 ; PRIOR APPLICATION NUMBER: US 60/292,599
 ; PRIOR FILING DATE: 2001-05-22
 ; PRIOR APPLICATION NUMBER: US 60/362,944

;; PRIOR FILING DATE: 2002-03-08
 ;; NUMBER OF SEQ ID NOS: 335
 ;; SOFTWARE: Patent in version 3.1
 ;; SEQ ID NO 104
 ;; LENGTH: 1503
 ;; TYPE: PRT
 ;; ORGANISM: Homo sapiens
 US-10-153-244-104

Query Match 33.5%; Score 2041; DB 12; Length 1503;
 Best Local Similarity 38.8%; Pred. No. 9,66-180;
 Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;

QY 26 GEVNFSGGKRGKGFVRVPSGAVSVLFDLLAEMLPAPNLVSLVGEOPFAMKSMWR 85
 DB 128 GDIVFTGSLQKVKYVRSQDTPSSVIYHLMTOHMGDLVDPNLLISVTGAKFNKKPRLK 187
 QY 86 DVLKRGVKAASOTAMITLSARVGLARHVGQARHDSLASTSTKRVAVAGASLGRV 145
 DB 188 SIFRRGLVKAQTTGAMITIGSGHTGVKMGVGEAVRDPSSSSYKEGELITIGVATWGTV 247
 QY 146 LHRRLIEAODEFPVHYEPEDDGSQGPLCSLDSNLSHFILVPSGPGKDDLTLELRLE 205
 DB 248 HRREGLIHPGSPFAEYILDEBG--QGNLTCLDSNHSFILDVDTHGQYGEIPLRTLE 306
 QY 206 KHISQRAQYGGTSGIEIPVLCCLVNGDPNTLERISRAVEQAPWLLVSGSGIADVLAA 265
 DB 307 KFISQTERGGV-AIKIPIVCVLEGGGGLHTIDNATTTNGTPCVAVGSGRADVIAQ 365
 QY 266 LVNQP--HLVPRKVAEKQ---FKKFPKSHFSMEIVAKTKLQNTSHQHLITVYDEQ 320
 DB 366 VANLVSDITISLQOKLSVFPQEMFET--FTESRIEWTKKIQDIVRRQLLTVFRBGK 423
 QY 321 EGSEELDTVILKALVKACKSHSQEPDYLD--ELKLAVAMDRVDIAKSEIFNDGVEMKSCD 379
 DB 424 DGQODVVALIOLALKASRSQDHFGHEMNDHOLKLAVANRRVDIARSEIFNDEMOMKPSD 483
 QY 380 LEEVNVDAIVSNKPEFVRLFVNDGADVADFLTYGRLQELYSVSRKSLFDLLQKQKEA 439
 DB 484 LHPMTAALISNKPEFVKLFLENGVQKKEFVTWDTLLYLENLDPSCLFHSKLQK----- 538
 QY 440 RLTLAAGLTQOAREPAPG--PASFLEHVSRYLKQFLDQACRGFYQDGRPGDRRR----- 492
 DB 539 -----LVDEPERACAPAPRLQMHHVAQVLRLELDFQPLPRRRHNDRLTLPLV 592
 QY 493 -----LEKGAKRPTGOKWLLDNOKSENPMRFLMAVLONHMAATYRWAGQ 542
 DB 593 PAVKLVNCGVSLRSGLYKSSGSHVT-----TMDPIRDLILWAIQNRRELGLIWAQSQ 646
 QY 543 EGVAAALAAKILKEMSHLETEAAR--ATREAKYERLADLFSECYNSSEARAFAL 599
 DB 647 DCIAAALAKSKILKELKEBEDTDSSEMLALAE--EYHRAIGVTECYRDEBAQKLL 705
 QY 600 VRRNRCKSTCTCLHATEADAKAFADHGVQAFLTRIWMGDMAGTPIRLIGAFLCAL 659
 DB 706 TRVSAMKCTTCLQALAEAKMKFVSHGCIQAFLTRKVMGQSLVNGMIRVTLCLAEPL 765
 QY 660 VYTNLTSEEARLPTGLEDLODDLSLDTKSPKLGOSRVELEYEARAGDGRPRAVF 719
 DB 766 LITGLISREK-----LQD-----VGTAA----- 786
 QY 720 LLTRNRKMGAPVTVFLGNVVMYFAFLFTYVLLVDRPPPGSGPEVTLFVNFVFLV 779
 DB 787 ---RARAFAPVAVVFNHILNLSYFAFLCPAVLVAVNDQPV---PSWECALYIMLFSLV 840
 QY 780 LEEIRQGFTEBDTHLVKKFTLYVGDNNKCDMAVILPIVGVTCRMPSAFAEGRTVLA 839
 DB 841 CEEMKQLFYDDECCIMKKAALYFSDFMNKLGVGAILLFVAGLTCRLIPATLYPERVILS 900
 QY 840 MDPMVFTLRILHIFAIHKLGPKIIVVERMKDVEFEFLSVMLVAAGVTTOALLHHD 899
 DB 901 LDFILFCRLMHIIFITISKLGKIIIVRKMADVFEFLFLAVVAVSGVAKOALLHNE 960

QY 900 GRLEWIFRRVLYRPLYQIFQIP--LDEIDEARVNC--THPLLEDSPSCPS----- 948
 DB 961 RRVDMLFRGAVYHSLTIFGQIDGVNPNBHCSPNGDPY---KPCPSDATQO 1016
 QY 949 --LYANMLVILLVTFLLVTVNVLMLNLIAMFSTTFQVVGQANMFKFQRYNLIVETHE 1006
 DB 1017 RPARPEWLTVLLCLLYLFTVILLNLIAMFNFTFOOVHETDOIMFQSHDLIEEYHG 1076
 QY 1007 RPALAPFILLSHSLTLRRVFKKEAEHKEHLEERDLPDLQOKVVTWETQKENFSLKM 1066
 DB 1077 RPAAPFPILLSHQPLFKRVVLTAKRKHQKKEKEEADLSMEITLYKENYLONR 1136
 QY 1067 EKRRRDSEGVLRKTAHRVDIARYL-----GGLNEDEKRIKLESQINYSVLVS 1118
 DB 1137 QFOQKQREQKIEDISNKVDAMVLDLDPKRSQSM---EQRLASLEQVAAQARALHM 1193
 QY 1119 VADVLAAQGGPRSSQHCESQVLAAD---HRGIDGHEQFG 1157
 DB 1194 IVRTLRAAGFSSEADVPTLASQKAAEBDAPRGKRTKEBDG 1235

RESULT 9

US-10-210-152-21
 ; Sequence 21, Application US/10210152
 ; Publication No. US20030162189A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A NOVEL TRP CHANNEL FAMILY MEMBER, LTRPC3
 ; FILE REFERENCE: D0171 NP
 ; CURRENT APPLICATION NUMBER: US/10/210,152
 ; PRIOR FILING DATE: 2002-08-01
 ; PRIOR APPLICATION NUMBER: US 60/309,544
 ; NUMBER OF SEQ ID NOS: 320
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 21
 ; LENGTH: 1503
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-210-152-21

Query Match 33.5%; Score 2041; DB 12; Length 1503;
 Best Local Similarity 38.8%; Pred. No. 9,66-180;
 Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;

QY 26 GEVNFSGGKRGKGFVRVPSGAVSVLFDLLAEMLPAPNLVSLVGEOPFAMKSMWR 85
 DB 128 GDIVFTGSLQKVKYVRSQDTPSSVIYHLMTOHMGDLVDPNLLISVTGAKFNKKPRLK 187
 QY 86 DVLKRGVKAASOTAMITLSARVGLARHVGQARHDSLASTSTKRVAVAGASLGRV 145
 DB 188 SIFRRGLVKAQTTGAMITIGSGHTGVKMGVGEAVRDPSSSSYKEGELITIGVATWGTV 247
 QY 146 LHRRLIEAODEFPVHYEPEDDGSQGPLCSLDSNLSHFILVPSGPGKDDLTLELRLE 205
 DB 248 HRREGLIHPGSPFAEYILDEBG--QGNLTCLDSNHSFILDVDTHGQYGEIPLRTLE 306
 QY 206 KHISQRAQYGGTSGIEIPVLCCLVNGDPNTLERISRAVEQAPWLLVSGSGIADVLAA 265
 DB 307 KFISQTERGGV-AIKIPIVCVLEGGGGLHTIDNATTTNGTPCVAVGSGRADVIAQ 365
 QY 266 LVNQP--HLVPRKVAEKQ---FKKFPKSHFSMEIDYRWKTKLQNTSHQHLITVYDEQ 320
 DB 366 VANLVSDITISLQOKLSVFPQEMFET--FTESRIEWTKKIQDIVRRQLLTVFRBGK 423
 QY 321 EGSEELDTVILKALVKACKSHSQEPDYLD--ELKLAVAMDRVDIAKSEIFNDGVEMKSCD 379
 DB 424 DGQODVVALIOLALKASRSQDHFGHEMNDHOLKLAVANRRVDIARSEIFNDEMOMKPSD 483
 QY 380 LEEVNVDAIVSNKPEFVRLFVNDGADVADFLTYGRLQELYSVSRKSLFDLLQKQKEA 439
 DB 484 LHPMTAALISNKPEFVKLFLENGVQKKEFVTWDTLLYLENLDPSCLFHSKLQK----- 538

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QY 440 RUTLAGTQOAREBPAG--PASFHEVSRYLKDPLDADACGFGYODGPGDRRR-----492
DB 539 -----VLVDEBERACAPARPLQMHNVAOVLRELDGFTOPLYRPRHRDRLLLPV 592
QY 493 -----AEKPAKPTGQKWLIDNOKSENPMRDLFLWAVLONRHEMATYWMAGQ 542
DB 593 PHVKLVNOGVSLSRYKSSGHVTF-----TMDPIRDLILWAIQNRRELGIIMASQ 646
QY 543 EGVAAALAACTIKEMSHLEAEAR--ATREAKYERLALDLFSECSNSSEAPAFLL 599
DB 647 DCIAAALACSKILKEISKEEDTDSSEMLALAE-EYEHRAIGVFTECRKDEBAQKLL 705
QY 600 VRNRNCSWKTCLHATEADAKAFPAHDGVOAFLTRIMWGDMAAGTPILRLGAFCLPAL 659
DB 706 TRVSAWKTCTLOLALBAKMKFVSHGIGQAFLTRKWMGQSLVNDGLMRVTLCLAPFL 765
QY 660 VYTNLIITSEAPLRTGLELDLDDLSLDTESPLYGLOSVEELVEAPRAQDGRPAVF 719
DB 766 LITGLISFEKRA-----LQD-----VGTAA-----786
QY 720 LITRKRKMGAVVTVFLGNVVMYFAFLFTVYLVLDPRPPQSGPRTVLYFVFTLV 779
DB 787 ---RARAFETAVVVFHNLISYFAFLCLFAYLVWDFQPV---PSWCECATYMLFSLV 840
QY 780 LEEIRGFTDEDTLVKKFTLYVGDNNMKCDMAIFLPIVGTGRMLPSAEAGRTVLA 839
DB 841 CEEMQOLFYPDECGIMKKAALYFSDFMKLDVGAILLFVAGLTRILPATLYRGRVILS 900
QY 840 MDMVFTLRLIHIFAIHQOLGPKIIVBERMKDVFFFLFSLVWLAVAGVTTQALLHPD 899
DB 901 LDFILFCLRLMHIIFISKTLGPKIIVKRMKDVFFFFLAVVVSFGVAQAILIHNE 960
QY 900 GLEWIFRRVLYRPLQIFGOIP--LDEIDARVNC---THPLLEDSPCSPS-----948
DB 961 RRVDMFLFGAVHSHLITFGQIPGYIDGVNFMENHCSFNGIDPY---KPKCSBDATQO 1016
QY 949 --LVANMVLILLVFLVTVNLVNLMLIAMFSYTFQVVOGNATMFWKFORNLIIVEYHE 1006
DB 1017 RPAPEWLVLLCLCTLTNTLLNLMLIAMFNITFQOQERTDOIMKQORIDLIEYNG 1076
QY 1007 RPAAPRFLILSHLSTLRRVFEKKEAENKREHLERDLPDLQKVVTWETVOKENFLSKM 1066
DB 1077 RPAAPRFLILSHLQFLIRVVLLKTPAKKHQOLKNLEKNEBAILLSWEIYUKENYLOVR 1136
QY 1067 EKRKRDSEGEVUKTAHRYDPIAKYL-----GGLREOEKRIKLESQINVCVLYSS 1118
DB 1137 QFOQORPEOKIEDISNKVDAMVDLDDLPKRSQSM---EORLASLEBOVAQOTARALHM 1193
QY 1119 VADVLAQGGPRSSQHCESQOLVAD---HRGSDGWEPG 1157
DB 1194 IYRTLRASGFSSEADVPTLASQKAAEERPAERPGKRTKEPG 1235

RESULT 10
US-10-007-706-1
; Sequence 1, Application US/10007706
; Publication No. US20020182635A1
; GENERAL INFORMATION:
; APPLICANT: Penner, Reinhold
; APPLICANT: Fleis, Andrea
; TITLE OF INVENTION: METHODS OF SCREENING FOR LTRPC2 MODULATORS
; FILE REFERENCE: A-70040-1/RTF/NBC
; CURRENT APPLICATION NUMBER: US/10/007,706
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/248,442
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/254,528
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1503

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-007-706-1

Query Match      33.5%; Score 2041; DB 14; Length 1503;
Best Local Similarity 38.8%; Pred. No. 9.6e-180;
Matches 459; Conservative 200; Mismatches 399; Indels 124; Gaps 23;

QY 26 GEVNGSGKKRGKRVPRVSPGAPBDFLLAEHNLPAFLVLSVGEBOFPAMKSMWR 85
DB 128 GDVFTGSLSQVKKIVRSQDTPSSVYTHMTQMGVLVNPILSVTGAKFMKPRLK 187
QY 86 DVLKRGKLVAAQSTGAMITLSALRVGLARHVGQAVRDSHASTSTKVRVAVAGMAGSLGRV 145
DB 188 SIFRGLVKAQVTTGAWIITGSHGVMKQGEAVRDPSSLSYKEGELITITGAVTWGTV 247
QY 146 LHRRLIEBAQEDFPVHYEPEDDGGSGPLCSLDSNLSHTLVBERPGPGDGLTELRLE 205
DB 248 HRREGLIHPTGSFPFEXVILDEBDG--QGNLTCLDSNHSHEILVDDGTHGGVGEIPLRTBLE 306
QY 206 KHISQORAGYGTGSIIEIPVLCILVNGDPNTLERISRAVEQAAFWLLVSGGIADVLAA 265
DB 307 KFISQTERGQV-AIKIPIVCVLEGGPGLHTIDNATTGCTPCVVEGSGRVADVIAQ 365
QY 266 LVNQP--HLVRYKVAEKQ---FKEKFPKHSWEDIVETKLLQNTSHQHLITVYDFEQ 320
DB 366 VANLPVSDITISLIQKLSVFFQEMFET--FTESRIVEWTKKIDIVRRQLLTVFRBGK 423
QY 321 EGSEELDVITLKALVYKAKSHSOEPDYLD-ELKLAVAMDRVDIKSEIFNGDVWKKSCD 379
DB 424 DGQODVDAVIAIQALIKASRSODHFGHEWMDQLKLAVMNRVDLARSIEFMDQWQKPSD 483
QY 360 LEEVWVDALSNKPEFVLFVNDGADVADPLTYGSLQELYSVSRKSLFLDLOKQBEA 439
DB 484 LHPITLALISVKEPEVFLFENGVOLEFETMDLTLYLENLUDSCIFSHKSLQK-----538
QY 440 RUTLAGTQOAREBPAG--PASFHEVSRYLKDPLDADACGFGYODGPGDRRR-----492
DB 539 -----VLVDEBERACAPARPLQMHNVAOVLRELDGFTOPLYRPRHRDRLLLPV 592
QY 493 -----AEKPAKPTGQKWLIDNOKSENPMRDLFLWAVLONRHEMATYWMAGQ 542
DB 593 PHVKLVNOGVSLSRYKSSGHVTF-----TMDPIRDLILWAIQNRRELGIIMASQ 646
QY 543 EGVAAALAACTIKEMSHLEAEAR--ATREAKYERLALDLFSECSNSSEAPAFLL 599
DB 647 DCIAAALACSKILKEISKEEDTDSSEMLALAE-EYEHRAIGVFTECRKDEBAQKLL 705
QY 600 VRNRNCSWKTCLHATEADAKAFPAHDGVOAFLTRIMWGDMAAGTPILRLGAFCLPAL 659
DB 706 TRVSAWKTCTLOLALBAKMKFVSHGIGQAFLTRKWMGQSLVNDGLMRVTLCLAPFL 765
QY 660 VYTNLIITSEAPLRTGLELDLDDLSLDTESPLYGLOSVEELVEAPRAQDGRPAVF 719
DB 766 LITGLISFEKRA-----LQD-----VGTAA-----786
QY 720 LITRKRKMGAVVTVFLGNVVMYFAFLFTVYLVLDPRPPQSGPRTVLYFVFTLV 779
DB 787 ---RARAFETAVVVFHNLISYFAFLCLFAYLVWDFQPV---PSWCECATYMLFSLV 840
QY 780 LEEIRGFTDEDTLVKKFTLYVGDNNMKCDMAIFLPIVGTGRMLPSAEAGRTVLA 839
DB 841 CEEMQOLFYPDECGIMKKAALYFSDFMKLDVGAILLFVAGLTRILPATLYRGRVILS 900
QY 840 MDMVFTLRLIHIFAIHQOLGPKIIVBERMKDVFFFLFSLVWLAVAGVTTQALLHPD 899
DB 901 LDFILFCLRLMHIIFISKTLGPKIIVKRMKDVFFFFLAVVVSFGVAQAILIHNE 960
QY 900 GLEWIFRRVLYRPLQIFGOIP--LDEIDARVNC---THPLLEDSPCSPS-----948
DB 961 RRVDMFLFGAVHSHLITFGQIPGYIDGVNFMENHCSFNGIDPY---KPKCSBDATQO 1016
QY 949 --LVANMVLILLVFLVTVNLVNLMLIAMFSYTFQVVOGNATMFWKFORNLIIVEYHE 1006

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Db      1017 RPAPEEWLTVLLCGLYLLFTNLLNLLNLLAMFNNTFOQOEFTDOIWKFORDLLEEYHG 1076
Qy      1007 RPALAPFILLSHLSLTLRVFEKEAENKREHLERDLPDLPQKVYMETVOKENFLSGM 1066
Db      1077 RPAAPFILLSHLDLFTKRVVLTKPAPKHKOLKKELENEAALLSMEIYIKENYLONR 1136
Qy      1067 EKRRDSEGEVLRTAHRVDFIAKYL-----GGLREQEKRIKLSQINVCVLVS 1118
Db      1137 OFOQOEKREKIEDISNKVDAMVLLDLDPLKRSMS--EQRSLSEQVAVQTRALHW 1193
Qy      1119 VADVLAOGGGRSSQHCSEGSQVLAAD--HGGIDGMEQPG 1157
Db      1194 IVRTLRASGFSSEADVPTLASQAAEEDPAEPGGRKTEEPG 1235

RESULT 11
US-10-171-319-8
; Sequence 8, Application US/10171319
; Publication No. US20030157633A1
; GENERAL INFORMATION:
; APPLICANT: Ardem Patapoutian
; APPLICANT: Andrea Peier
; APPLICANT: Peter McIntyre
; APPLICANT: Stuart Bevan
; APPLICANT: Chuansheng Song
; APPLICANT: Pamposh Ganju
; TITLE OF INVENTION: VANILLOID RECEPTOR-RELATED NUCLEIC ACIDS
; TITLE OF INVENTION: AND POLYPEPTIDES
; FILE REFERENCE: 4-32048A
; CURRENT APPLICATION NUMBER: US/10/171,319
; PRIOR FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/297,835
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: 60/351,238
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/352,914
; PRIOR FILING DATE: 2002-01-29
; PRIOR APPLICATION NUMBER: 60/357,161
; PRIOR FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: 60/381,086
; PRIOR FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/381,739
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1104
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-171-319-8

Query Match      25.9%; Score 1578; DB 12; Length 1104;
Best Local Similarity 33.4%; Pred. No. 6.5e-137;
Matches 374; Conservative 207; Mismatches 392; Indels 148; Gaps 24;

Qy      26  GGVNNGSGKKRGKRVVPSGVAASVLFLLAEWHLPAPNVVSLVGEDEQFAMKSLR 85
Db      104  GDIOPTLGGK-GKTLRLSCDTSETLYELLQHWHLTPNLVLSVTGAKNFALPKPRMR 162
Qy      86  DVLRKGLVKAQSTGAWILTSALRVGLARHVGQAVRSHSLASTSTKRVAVVAGMASLGRV 145
Db      163  KIFSR-LIYIAQSKAWILTGTHGLMKYIGEVVNDNTI--SRNSEINIVALIGIAMGV 220
Qy      146  LHRRLLEAQRD--FPHYFEDDGGSGQPLCSLDSNLSHTLVBPFGPKGDLTELR 202
Db      221  SNRPTLRSCDEGHFSAQYIMDD-FTRDPLYILDNNHTHLVYDNGCHGHPVEAKLRN 279
Qy      203  RLEKHSIE---QRAGYGTGSIETIPVLCILVNGDNTLERISRAVEQAAPMLIVGSGGI 259
Db      280  QLEKISRTSDSNVYG---KPIVFPAGGGGSETIKAINTSVSKIPCVVVEGSGOI 335
Qy      260  ADVLAALVNPHLVLPKVAEKQFKKFPSS--KHFSWEDIIVWTKLQNTISHOHLTVYD 317

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Db      336  ADVIASIVEVDVLTSSMWKEKLVRFLEPRTVSRLPEEIEBSWIKWLKEISSHLLTYIK 395
Qy      318  FEOGSEEDLVYILKALVKACKSHQOEQDYLDELKLAVANDRVDAIASEIFNGEVKMS 377
Db      396  MEAGDEIVSAISALYALKASTNEQDKONNNGQIKLENNQDLDADEFTNDRWES 455
Qy      378  CDLEEVVDALVSNKPEFVRFLVNGADVADVAFLYGRLOEYRSVRSKSLFDLLQ---R 434
Db      456  ADLQGVMTALIKORPKRVRLFLNGNLQKFTLNEVTELF-SHSEFTLVYRNQIAKN 514
Qy      435  KOBEARLTLAGLGTQOAREPAPGAPFSLHEVSRVLCFLODACGFYQDGRPGDRRAE 494
Db      515  SYNALLTF-----VWKLVANFR---RSFWKEDR----- 540
Qy      495  KGPARKPTGQKMLDLNOKSENPMWRDLFLMAVLONRHEMATYFPAMQGEQVAAALAAKI 554
Db      541  ---SSREDLVLDASLTTHPLQALFTWAILQNKELSVIWEQTGCTLLAALGASKL 597
Qy      555  LKEMSHLETEAARATREA--KYERLADLFSECEYSSEARAFALVRRNRCSKTTCL 612
Db      598  LKTLAKVNDINNAQSESELANYETRAVELFTECYSNDEDLAQLLVYSCBAGSNCCL 657
Qy      613  HLATEADAKAFPAHDGVAFLTRIMWGDMAAGTPILRLLAGFLCPALVYTNLITFSEAP 672
Db      658  ELAVEATDQHFIAQPGVQNFSLKQWYGBISRDYKWKIILCLFTIPLVCGGLVSPKK-- 715
Qy      673  LRTGLEDLQDLSIDTESPIYGLQSRVLELVEAPRAQDGRPAVFLITRRKRWGAPV 732
Db      716  -----PIDKHK-----LLWYVAFETSPF 735
Qy      733  TVPLGNVVMYPAFLFTYVLLVDFRPPQSGSEVTLVFWVFLVVEEIRQGFTEDE 792
Db      736  VVFSNVMVFYAFLLFPAYVLLMDFHSVPH--TPELLVLLVFLPCDEVRQMYMGVN 792
Qy      793  THLVKKFTLVYGDNNKCDMAVIFLFIYVTCRM---LPSAFBAGRTVLANDFVFTLR 849
Db      793  -----YPTDLMNVMDTLGLFYFIAGIYFRLHSSKSLSGRVIFCDYIIFTRL 843
Qy      850  ITHFAIKQGPKIIVVERMKVDVFFPLFSLVNLVAVGVTQALLHHDGRLEIFRRV 909
Db      844  IHIFTVSRNLGPKIMQRMIDVFFFLFPAVWVAFGARQGLRLRNEQRMWRIFRSV 903
Qy      910  LYRPYLOFGQIPDEIDEARVNC-----THPLLE-DSPSCPSLVANMLITLLV 960
Db      904  IYEPYLMFGQVPSD-VDSTTYDSHCTFSGNEKSPCLVEIDENHLPR-FEWITIPVLC 961
Qy      961  TFLVTVLNLNLLIAMESYTFQVVGATMFMKFORNYNLIVEYHERPALAPFILLSHL 1020
Db      962  IYMLSTNILLVNLVAMFGYVGVQENNDQVMKFORFLVQVQCNRLNIFFPFVFAVYF 1021
Qy      1021  SLTRRVFKKAENKREHLERDLPDLPQKVYMETVOKENFLSKMKERRRDSGEVLAK 1080
Db      1022  YMVVKKCFKCCCKEKNMESNACCFRNEBNETLAMEGWKENYLVKINTKANDNS----- 1075
Qy      1081  TAHRVDFIAKLGRLREQEKRIKLSQINVCVLVSVD 1121
Db      1076  -----EEMRRHFRQDLSKLANDKSLKLEIAN 1101

RESULT 12
US-09-759-143-778
; Sequence 778, Application US/09759143
; Patent No. US2002022248A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.

```


APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepier, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 778
LENGTH: 1095
TYPE: PRF
ORGANISM: Homo sapiens
US-09-759-143-778

Query Match 25.7%; Score 1562.5; DB 9; Length 1095;
Best Local Similarity 34.2%; Pred. No. 1.8e-135;
Matches 378; Conservative 202; Mismatches 394; Indels 131; Gaps 27;

26 GEVNGSGGKRRGKRVPSVAVPVLFDLLAEMHLPAPNLVSLVGEOPFANKSMWR 85
95 GDIOFETLGRK-GKYIRLSCDTDAELTYELLTOHMLKLPNLVISTGAKNFALPRMR 153
86 DVLRLGVLKAAQSTGAMITLSALRVGLARHVGAVDHSLASTSTKRVAVVAGMASLGRV 145
154 KIFSR-LITIAOSKAMITGTHGLTYIGEVARDNT-SRSEENIVALGIANAMGV 211
146 LARRILE--EAQEDFPVHYRPPDDGSGGRLCSLDSNLHFLVBERPGKDGLETLRL 202
212 SNRDTLRNCDAEGYLAQYLMDD-FTRDPLYLDNNHHTLLVNDGCHGPTVEAKLEN 270
203 RLEKHTISE--ORAGVGTSIEIPULCLLVNDPRTLEIRISRAVGOAPMLIVGSGGI 259
271 QLEKHTISETTIDSNVG--KIPVCPAOGGKETTIAINTSINKLPCVVVBESGKI 326
260 ADVLALVNPPLHLPVKAQKFEKEFP--KHFSMEDIVRWTKLONITSHOHLITVVD 317
327 ADVIASLVEDEAPRTSSAVKEKLVRLPTVSRLSEETRESIKMLKEITLCSHLLTVRK 386
318 FEQESSELDVTYLKALVYACKSHSQEPDYLDELKLAVAMRDVIAXSEIFNGDVEMKS 377
387 MEAGDEIVSNALSYALYKAFSTSEODKUNWGQLKLLLEMMQDLANDEIFTNDRMES 446
378 CLEBYMVDAVSNKEPFRFLVDNCAVDADFLTYRLOELYRSVRKSLDLDLO--R 434
447 ADLOEVMFALIKDRKFRFLLENGLNLRKELTHVLTFLF-SNHFSTLVRRNLQIAN 505
435 KOBEARLITLAGTQOARPPAPRPAFSLSHEVSRVLDKFLQDARCFYDGGPRG-DRRA 493
506 SYNDALITL-----VKLVANR-----KGRKEDNRGRBEMTI 539
494 EKGPAKRPFGOKWLLDNOKSEPMWDLFLMAVLONRHMAFYFWAMGEGVAAALAAK 553
540 E-----LHDVSPITRHPLOALFIMAILQKKELSKYIMBOTRGCTLAALGASK 587
554 ILKEMSHLETEAARATREA--KYERLALDLSFECYSNSEARAFLLVRRRCWMTKC 611
588 LKTLAKVNDINNAESELNEVETRAVELFTECYSDDEDLAELVYSCGAWGNSNC 647
612 LHLATEADAKAFADGVQAFILTRIMWGMAAGTPIRLIGAFALCALVYTNLITSEEA 671
648 LELAVATQHTAOGVONFLSKQYGEISBDTKMKIILCIFIPLVCGGCVSRKK- 706
672 PLRTGLIEDLDLSTDEKSPLYGLQSRVEELVAPRAQDRPRAVFLITRMRKFWGAP 731
707 -----PVDKHKK-----LLWYVAFFTSP 725

732 VTVFLGNVWYAFPLFTYVLVNDFRPPQSGSEVTLFWFTLVLEIRQGFIDE 791
726 FVPSMNWVFIARILLFAYVLDNDHVPVH--PRELVISLVFLVLCDEVRQWYVNGV 782
792 DTHLVKKEFTLVYDGNMKNCDVAIFLIVGTCRN--LPSAFAEGRTVLANDENVFTLR 848
783 N-----YFTDLMMVDTLGLFVFIAGIVFRLSHSNKSLYSGRAVIFCLDYIIFTLR 833
849 LIHIFAIHKOQPKTIIVERMMKOVFFPLFSLVSLVAVGTTQALLPHORLEMRIR 908
834 LIHIFTVRNIGPKTIMQRMIDVFFPLFPAVMMVAFGARQGLKONEGRMWRIFS 893
909 VLYRPIYIFGOIPLDEIDEAR--VNCS-----THPLLE-DSBSCPSLYANMLVILL 959
894 VLYRPIYLMFGVOPD-VDGTTYDPAHCTFPGNESKPLCEVLEIDENLDR-FREWITIPV 951
960 VTFLVTVLNNLNLIAFSTYFOVYOGNATFMKFORNVLIVEYHERPALAPPTILSH 1019
952 CIYMLSTWILLVNLVAMEGTVGVOENNDQVMKFORVFLVQESRLNIPFPPIVAY 1011
1020 LSLTRRVFKAEKREHLERDLPDLDOKVYVMEYQKENVLSKMKRRDRSGEVL 1079
1012 FYMVVKKCFCKCKEKNNESSVCCEKBNEDNELLAMEGWKENYLVKINTKANDT-SEEMR 1070
1080 KTAHRVDFIAYLGS-LRQOEKRIK 1103
1071 HRFRODTKNDLKLKEINANKIK 1095

RESULT 13
US-09-780-669-778
Sequence 778, Application US/09780669
Patent No. US20020051977A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, David C.
APPLICANT: Mitchell, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yugu
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darriek
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yaelir A.W.
APPLICANT: Hepier, William
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
NUMBER OF SEQ ID NOS: 943
CURRENT FILING DATE: 2001-02-09
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 778
LENGTH: 1095
TYPE: PRF
ORGANISM: Homo sapiens
US-09-780-669-778

Query Match 25.7%; Score 1562.5; DB 9; Length 1095;
Best Local Similarity 34.2%; Pred. No. 1.8e-135;
Matches 378; Conservative 202; Mismatches 394; Indels 131; Gaps 27;

26 GEVNGSGGKRRGKRVPSVAVPVLFDLLAEMHLPAPNLVSLVGEOPFANKSMWR 85


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Db      95 GDIQETLGGK-GKTYRLSCDTDAEILYELLTOHMLKTPNLVLSVTGAKNFALKPRMR 153
Qy      86 DVLKGLVKAAGSTGAMILTSALRVGLARHVQAVRDSLASTSTKRVAVNAGASLGRV 145
Db      154 KIFSR-LIYIAQSGAMILTCGTHGLTKYIGEVVRNTI-SRSEENIYVAIGIAMGMV 211
Qy      146 LHRRL--EAQEDFPVHYREDGSGQPLCSLDSNLSHFILVEPRPGKDGTELRL 202
Db      212 SNRDTLRNCDAEGYFLAQYLMDD-FTRDPLIYIDNNHTHLLVDNCGHGTVEAKLRN 270
Qy      203 RLEKHISE--ORAGYGTGSIETPVLCVLVNGDNTLERISRAVEQAAPMLILVSGGI 259
Db      271 QLEKHISERTTQDSNYG--KIPVCFAGGKETLKAINTSIKKKIPCVVEGSGRI 326
Qy      260 ADVLAALVNOPHLLVPKVAEKQFEKPPS--KHFSMEDIVRWTKLONITSHOHLTYVD 317
Db      327 ADVIASLVEEDAPTSSAVKEKLVRLPRYVSRLSSEETESWIKMLKEILCSHLITVYK 386
Qy      318 FEQSGSELDTVIILKALVKACKSHSQEPQDYLDLKLAVANDVIAKSEIFNGDVEWKS 377
Db      387 MEEAGDEIVSNASIALYKAFSTSEQDKNNNGQLKLLBNQDLANDEIFTNDRWES 446
Qy      378 CDLEBWVDAVLSNKEPFRVLFVNDGADVADPLTYGRLQELYSVRSKSLFDLQ--R 434
Db      447 ADLQEVMTALIKRPFVRLFLENGLNRKFLTHDVLTELF-SNHFSTLYRYMLQIAKN 505
Qy      435 KOEABRLTLAGLQOAREPPAGPAPFSLHEVSRVLCFLODACGFGDOPG-DRRA 493
Db      506 SYNDALITF-----VKLVANFR---RGFKEDNCRDENDI 539
Qy      494 EKGPAPRTGQKWLIDLNOKSENPWRDLFLMAVLONRHEMATYFWAMQOEGVAAALACK 553
Db      540 E-----LHDVSPITRHPLOALFIWAILONKKELSKVIMEQRTGCTLAALGSK 587
Qy      554 ILKEMSHLETAEARATREA--KYERLADLFSCYSNSBARFALLVRRNRCKSTTC 611
Db      588 LKTLKAVKNDINAGSEBELANEYETRAVELFTECVSSDEDLAEQLLVYSCAMGSGNC 647
Qy      612 LHLATEADAKAFPAHDVQAFLTRIMGDMAGPILRLGALFCFALVYTNLITFSEA 671
Db      648 LELAVEATDQHTAQOPVQNLFSKOMYGEISBDTKMKIILCFITPLVCGFVSFKK- 706
Qy      672 PLRTGLBDLQDLSDTEKSPLYGLQSRVEELVEAPRAQDGRPAVFLTLTRMKFWGAP 731
Db      707 -----PVDKHK-----LMWYVAFFTSP 725
Qy      732 VTFVLGNVWVFAPFLFTTYLLVDFRPPQSGSGEVTLYFWFTLVLEIRQGFTE 791
Db      726 FVFSWNVVFIATLLFAVYLLMDFHSPH---PPELVLSLVFLFCDEVRQMYVNGV 782
Qy      792 DTHLVKKFTLVGNMNCMDVVAIFLFIYVTCRM---LPSAFEGGRVVLAMDENVFTLR 848
Db      783 N-----FTDLMNVMDTLGLFYTAGIVFRHSSNKSLSGRIYFLCLDIIFLRL 833
Qy      849 LHHFAIHKQAPKIIIVERMMKDVFFFLFSLVWLVAVYVTOALLPHDGRLEWIFRR 908
Db      834 LHHFTYSRNLGPKIIMQRLIDVFFFLFPAVMMVAFVARGCILRQNRKRMIFRS 893
Qy      909 VLYRPYQIFQOILDEIDEAR---VNC-----THPILLE-DSPSCSLVANNLVILL 959
Db      894 VLYRPYLAHQVQPSD-VDTTYVFAHCTFGNESPCLVLELDEHNLEPR-PREMITPLV 951
Qy      960 VTFPLVNVLLMNLILMFSTYPOVONATMFWKFOQVNLIVYHERPALAPFILLSH 1019
Db      952 CIYMLSTNILLVNLVAMFGITVGTVDENNQVMPFORYFLVQECSSNLPPFIFAY 1011
Qy      1020 LSLTLREVFKKAEKHEHLERDPLDQKVVTWETVQENFLSKMEKRRRDSGEVLR 1079
Db      1012 FYWVWVCKFCCKCKEKNNESSVCCFKNEDNETLAMEGWKENYLVKINTKANDI-SEMR 1070
Qy      1080 KTAHRVDPFIATYLG-LREQEKRIK 1103

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Db      1071 HRFQDLTKMLDKLLEKIANKIK 1095

RESULT 14
US-09-822-827-778
; Sequence 778, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822, 827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 778
; LENGTH: 1095
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-822-827-778

Query Match      25.7%; Score 1562.5; DB 9; Length 1095;
Best Local Similarity 34.2%; Pred. No. 1.8e-135;
Matches 378; Conservative 202; Mismatches 394; Indels 131; Gaps 27;

Qy      26 GEVNFSGGKRGKGFVPRPSVAPVLPDLLAEMLPAPLVYSLVGEQPFAMKSWLR 85
Db      95 GDIQETLGGK-GKTYRLSCDTDAEILYELLTOHMLKTPNLVLSVTGAKNFALKPRMR 153
Qy      86 DVLKGLVKAAGSTGAMILTSALRVGLARHVQAVRDSLASTSTKRVAVNAGASLGRV 145
Db      154 KIFSR-LIYIAQSGAMILTCGTHGLTKYIGEVVRNTI-SRSEENIYVAIGIAMGMV 211
Qy      146 LHRRL--EAQEDFPVHYREDGSGQPLCSLDSNLSHFILVEPRPGKDGTELRL 202
Db      212 SNRDTLRNCDAEGYFLAQYLMDD-FTRDPLIYIDNNHTHLLVDNCGHGTVEAKLRN 270
Qy      203 RLEKHISE--ORAGYGTGSIETPVLCVLVNGDNTLERISRAVEQAAPMLILVSGGI 259
Db      271 QLEKHISERTTQDSNYG--KIPVCFAGGKETLKAINTSIKKKIPCVVEGSGRI 326
Qy      260 ADVLAALVNOPHLLVPKVAEKQFEKPPS--KHFSMEDIVRWTKLONITSHOHLTYVD 317
Db      327 ADVIASLVEEDAPTSSAVKEKLVRLPRYVSRLSSEETESWIKMLKEILCSHLITVYK 386
Qy      318 FEQSGSELDTVIILKALVKACKSHSQEPQDYLDLKLAVANDVIAKSEIFNGDVEWKS 377
Db      387 MEEAGDEIVSNASIALYKAFSTSEQDKNNNGQLKLLBNQDLANDEIFTNDRWES 446
Qy      378 CDLEBWVDAVLSNKEPFRVLFVNDGADVADPLTYGRLQELYSVRSKSLFDLQ--R 434
Db      447 ADLQEVMTALIKRPFVRLFLENGLNRKFLTHDVLTELF-SNHFSTLYRYMLQIAKN 505
Qy      435 KOEABRLTLAGLQOAREPPAGPAPFSLHEVSRVLCFLODACGFGDOPG-DRRA 493
Db      506 SYNDALITF-----VKLVANFR---RGFKEDNCRDENDI 539
Qy      494 EKGPAPRTGQKWLIDLNOKSENPWRDLFLMAVLONRHEMATYFWAMQOEGVAAALACK 553
Db      540 E-----LHDVSPITRHPLOALFIWAILONKKELSKVIMEQRTGCTLAALGSK 587
Qy      554 ILKEMSHLETAEARATREA--KYERLADLFSCYSNSBARFALLVRRNRCKSTTC 611
Db      588 LKTLKAVKNDINAGSEBELANEYETRAVELFTECVSSDEDLAEQLLVYSCAMGSGNC 647
Qy      612 LHLATEADAKAFPAHDVQAFLTRIMGDMAGPILRLGALFCFALVYTNLITFSEA 671
Db      648 LELAVEATDQHTAQOPVQNLFSKOMYGEISBDTKMKIILCFITPLVCGFVSFKK- 706
Qy      672 PLRTGLBDLQDLSDTEKSPLYGLQSRVEELVEAPRAQDGRPAVFLTLTRMKFWGAP 731
Db      707 -----PVDKHK-----LMWYVAFFTSP 725

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QY 732 VTVELGNVMMYFAFLFTYVLLVDFRPPGSGSEVTLVFWVTLVLEBIRGFFTDE 791
 DB 726 FVFSMNVVFIYAFLLFAVYLLMDPHSVPH---PPELVLSLVVLFCDEVRQVYVNGV 782
 QY 792 DTHLVKFKETLVYGDNMNKCDAVAIFLFTVGTCRM---LPSAFEAGRTVLAMDENVFTLR 848
 DB 783 N-----YFTDLMNVMDTLGLFYFIAGIYFRLHSSNKSLSYSGRAVIFCLDYIIFTLR 833
 QY 849 LHIHFAIHKQCGPKTIIVBRMKKDVFFFLFSLVSLVAVGTTQALLPHDGRLEWIRRR 908
 DB 834 LIHIFTVSRNLGPKIIMQRMIDVFFFLFPAVMVAVFGVARQOILRNEGRMWMIFRS 893
 QY 909 VLYRPLYOIFGOIPLDEIDEAR---VNCs-----THPLLE-DSPSCSLVANMVLVILL 959
 DB 894 VLYRPLYLNFQGVPSD-VDGTYYDPAHCTFTGNESEKPLCVELDENHNR-PEWITIPLV 951
 QY 960 VTFLVTLVNLMLNLIMAFESYTFQVVGATMFKFORYNLIVEYHERPALAPPELLSH 1019
 DB 952 CIYMLSTNILLVNLVAMFGYTVGQENNDQVMKFORFLVQVCSRLNIFPFLIVAFY 1011
 QY 1020 LSLTRRVFKKAHKEHLEHLEDPDLDQKVVTMETVQKENPLSKMEKRRDSEGEVLR 1079
 DB 1012 FYMVVKKCFKCCCKEKNNESSVCCFKNEDETILAMEGVKENVLYKINTKANDT-SEEMR 1070
 QY 1080 KTAHVDPLAKYLG-LRQEKRIK 1103
 DB 1071 HRFROLDTKLNDLKGLEIKANKIK 1095

RESULT 15

US-09-895-793-778
 ; Sequence 778, Application US/09895793
 ; Publication No. US20020192763A1

; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitchem, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yugu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Reiter, Marc W.
 ; APPLICANT: Stolk, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aljun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Basols, Carlotia
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; FILE REFERENCE: 210121.534C2
 ; CURRENT APPLICATION NUMBER: US/09/895,793
 ; NUMBER OF SEQ ID NOS: 982
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 778
 ; LENGTH: 1095
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-895-793-778

Query Match 25.7%; Score 1562.5; DB 10; Length 1095;
 Best Local Similarity 34.2%; Pred. No. 1.8e-135;
 Matches 378; Conservative 202; Mismatches 394; Indels 131; Gaps 27;

QY 26 GEVNFSGGKRGKFRVPSGVAPSLVEDLLAEWHLPAPNLVSLVGEOPFAMKSWLR 85
 DB 95 GDIFQETLGGK-GKTIKRLSCDTDAEILYELLTQMHMLKPTPLVLSVTCGACGNFALKPRMR 153
 QY 86 DVLKRGVKAQAOSTGAMITLSALRVLARHVGQAVRDSLASTSTKRVAVVAGASLGRV 145
 DB 154 KIFSR-LIYIQAOSKAMILLTGTHGLTKYIGEVNRDWTI-SRSSEENIIVAIIGIAAMGV 211
 QY 146 LHRRL-BAQEDFPVHYPEDDGGSGGCLSDNSHSHLIVEGPGGDDGLELR 202
 DB 212 SNRDTLRNCDAEGVFLAQYLMDD-FTDPVLIIDNNHTHLLVDNGHGHPTVEAKLN 270
 QY 203 RLEKHISE---ORAGYGTGSIIEIPVLCILVNGDPNTERISRRAVEQAPMLILVSGGI 259
 DB 271 QLEKHISRTIODSYGG---KPIYVCFAGGCGGETIKALINTSIKNI PCVVVSGSRI 326
 QY 260 ADVLAALVNOPLLVPKVAEKQFEKFPSS-KHFSMEDIVWTKLLQNTSHOHLTYVD 317
 DB 327 ADVIASLVEVDAPTSAAVKEKLVRFPRVTSRLSEETESMIKWLKEILCSHLLTVIK 386
 QY 318 FEQSGSEELDTVILKALVKACKSHQEPQDYLDLKLAVANDRVDIASEIFENGVEKS 377
 DB 387 MEEAGDEIVSNAISYALYKASTSEODDNNGQKLLLENNQDLANDELFTNDRWES 446
 QY 378 CDLEEVMDALVSNKEFEVRLFVNDGADVADFLTYGRLOEYRSYSRSLSFLDLQ---R 434
 DB 447 ADLQEVMTALIKDRPKFVRLFLENGLNRKFLTHDVULTELF-SHNESTLYVRNIQIAKN 505
 QY 435 KOEBARLTLAGLGTQOAREPPAGPAPFSLHEVSVLKDLODACGFYODGPPG-DRRRA 493
 DB 506 SYNDALLTF-----VWKLVANFR---RGFRKEDRNGRDEMNDI 539
 QY 494 EKGPARKPTGQKMLDLNOKSENPRDLFLVAVLONRHEMATYFAMQOEGVALLAAACK 553
 DB 540 E-----LHDVSPITRHPLOALFVIAIIONKKELSLVWEQTRGCTLALGASK 587
 QY 554 ILEKWSHLETEAARATREA--KYERLALDIFSECSYNSSEARFALLVRRNRCSKTYTC 611
 DB 588 LKTLAKKXNDINMAGESEBELANETRYAVELFTCTCYSDDELAAQLLVYSGEAMGSGNC 647
 QY 612 LHLATEADAKAFPAHDVQVAFTRIMWGDMAAGPILRLGALFCALVYTNLTFSEBA 671
 DB 648 LELAVEATDQHTAOPGVQNFSLKQWGEISBDTGMKIIILFLIPLVGCFSVFRKK- 706
 QY 672 PLRTGLEDLDLSDTDEKSPLYGLOSRVBEIVLRPAQDGRPAVLLITMRKMGAP 731
 DB 707 -----PVDKKKK-----LWYVAFFTSP 725
 QY 732 VTVELGNVMMYFAFLFTYVLLVDFRPPGSGSEVTLVFWVTLVLEBIRGFFTDE 791
 DB 726 FVFSMNVVFIYAFLLFAVYLLMDPHSVPH---PPELVLSLVVLFCDEVRQVYVNGV 782
 QY 792 DTHLVKFKETLVYGDNMNKCDAVAIFLFTVGTCRM---LPSAFEAGRTVLAMDENVFTLR 848
 DB 783 N-----YFTDLMNVMDTLGLFYFIAGIYFRLHSSNKSLSYSGRAVIFCLDYIIFTLR 833
 QY 849 LHIHFAIHKQCGPKTIIVBRMKKDVFFFLFSLVSLVAVGTTQALLPHDGRLEWIRRR 908
 DB 834 LIHIFTVSRNLGPKIIMQRMIDVFFFLFPAVMVAVFGVARQOILRNEGRMWMIFRS 893
 QY 909 VLYRPLYOIFGOIPLDEIDEAR---VNCs-----THPLLE-DSPSCSLVANMVLVILL 959
 DB 894 VLYRPLYLNFQGVPSD-VDGTYYDPAHCTFTGNESEKPLCVELDENHNR-PEWITIPLV 951
 QY 960 VTFLVTLVNLMLNLIMAFESYTFQVVGATMFKFORYNLIVEYHERPALAPPELLSH 1019
 DB 952 CIYMLSTNILLVNLVAMFGYTVGQENNDQVMKFORFLVQVCSRLNIFPFLIVAFY 1011
 QY 1020 LSLTRRVFKKAHKEHLEHLEDPDLDQKVVTMETVQKENPLSKMEKRRDSEGEVLR 1079
 DB 1012 FYMVVKKCFKCCCKEKNNESSVCCFKNEDETILAMEGVKENVLYKINTKANDT-SEEMR 1070

Wed Sep 10 09:59:28 2003

us-09-834-792c-4.rapb

Page 13

Qy 1080 KTAHRVDFIAKYLGG-LREQEKRIK 1103
Db 1071 HRFROLDPTLNDLKGILKEIANKIK 1095

Search completed: September 10, 2003, 09:47:00
Job time : 37 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2003, 09:30:34 / Search time 46 Seconds
(without alignments)
6535.463 Million cell updates/sec

Title: US-09-834-792C-4

Perfect score: 6051
Sequence: 1 MODVGGPRPGSGDAEDRRR.....HRGGIDGWEQPGAGQPPSDT 1165

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	6073	99.7	1165	4 Q9NZQ8	Q9NZQ8 homo sapien
2	6019	98.8	1159	4 Q9NY34	Q9NY34 homo sapien
3	5068.5	83.2	1158	11 Q9JUH7	Q9JUH7 mus musculus
4	5018.5	82.4	1148	11 Q9EPM4	Q9EPM4 mus musculus
5	5008.5	82.2	1148	11 Q9NPF9	Q9NPF9 mus musculus
6	4963.5	81.5	1116	11 Q9EPM3	Q9EPM3 mus musculus
7	4445.5	73.0	1030	11 Q8BS44	Q8BS44 mus musculus
8	2430.5	33.9	1214	4 Q8TD43	Q8TD43 homo sapien
9	2166.5	35.6	1040	4 Q96L84	Q96L84 homo sapien
10	2146	35.2	1016	4 Q9NXXV1	Q9NXXV1 homo sapien
11	2051	33.7	945	11 Q8BLM7	Q8BLM7 mus musculus
12	2024	33.2	1507	11 Q91YD4	Q91YD4 mus musculus
13	1578	25.9	1104	11 Q8RAD5	Q8RAD5 mus musculus
14	1563.5	25.7	1104	11 Q8RAD5	Q8RAD5 mus musculus
15	1559.5	25.6	1095	4 Q8TDX8	Q8TDX8 homo sapien
16	1559.5	25.6	1104	4 Q8TAC3	Q8TAC3 homo sapien

17	1228.5	20.2	1533	4 Q75560	Q75560 homo sapien
18	1208.5	19.8	1862	11 Q925B2	Q925B2 mus musculus
19	1208.5	19.8	1863	11 Q923J1	Q923J1 mus musculus
20	1208.5	19.8	1863	11 Q9JLQ1	Q9JLQ1 mus musculus
21	1183.5	19.4	1864	4 Q9BXR2	Q9BXR2 homo sapien
22	1183.5	19.4	1865	4 Q96QT4	Q96QT4 homo sapien
23	1174.5	19.3	2022	4 Q9BX84	Q9BX84 homo sapien
24	1157	19.0	2028	11 Q8CIR4	Q8CIR4 mus musculus
25	1141	18.7	1131	5 Q9V7A5	Q9V7A5 dirosophila
26	1139.5	18.7	686	6 Q8HXH2	Q8HXH2 macaca fasc
27	1113.5	18.3	485	11 Q9ES05	Q9ES05 rattus norv
28	1064	17.5	1971	5 Q8IG04	Q8IG04 caenorhabdi
29	1062	17.4	2032	5 Q9J971	Q9J971 caenorhabdi
30	1048	17.2	1078	5 Q8MLA4	Q8MLA4 dirosophila
31	990	16.3	1363	5 Q20766	Q20766 caenorhabdi
32	887.5	14.6	1681	5 Q8IG05	Q8IG05 caenorhabdi
33	881	14.5	1707	5 Q17652	Q17652 caenorhabdi
34	874.5	14.4	1133	4 Q9H637	Q9H637 homo sapien
35	863	14.2	848	11 Q8BIH6	Q8BIH6 mus musculus
36	818	13.4	1122	5 Q8IG06	Q8IG06 caenorhabdi
37	687.5	11.3	737	11 Q8BJ11	Q8BJ11 mus musculus
38	593	9.7	515	11 Q8C787	Q8C787 mus musculus
39	564	9.3	575	4 Q9HXQ2	Q9HXQ2 homo sapien
40	498	8.2	542	11 Q703J4	Q703J4 mus musculus
41	458.5	7.5	640	6 Q9GMW4	Q9GMW4 macaca fasc
42	360	5.9	372	11 Q9CUT2	Q9CUT2 mus musculus
43	349	5.7	338	4 Q9H200	Q9H200 homo sapien
44	341.5	5.6	361	11 Q8BI66	Q8BI66 mus musculus
45	341.5	5.6	369	11 Q8BK11	Q8BK11 mus musculus

ALIGNMENTS

RESULT 1

ID	Q9NZQ8	PRELIMINARY:	PRT:	1165 AA.
AC	Q9NZQ8;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)			
DE	MTR1.			
GN	MTR1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20076317; PubMed=10607831;			
RA	Pravitt D., Enkhar T., Klemm G., Gaertner B., Spangenberg C.,			
RA	Winterpacht A., Higgins M., Pelletier J., Zabel B.,			
RT	"Identification and characterization of MTR1, a novel gene with			
RT	homology to melastatin (MLSN1) and the tip gene family located in the			
RT	BMS-WT2 critical region on chromosome 11p15.5 and showing allele-			
RT	specific expression."			
RL	Hum. Mol. Genet. 9:203-216(2000).			
DR	EMBL; AF177473; AAF26288.1; --			
DR	GeneW; HGNC:14323; TRPM5.			
DR	InterPro; IPR002111; Cat_channel_Trl.			
DR	InterPro; IPR005821; Ion_trans.			
DR	Pfam; PF00520; ion_trans. 1.			
KW	ionic channel; Transmembrane.			
SQ	SEQUENCE 1165 AA; 131450 MW; C4AD5BAA866BE73B CRC64;			

Query Match 99.7%; Score 6073; DB 4; Length 1165;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1162; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MODVGGPRPGSGDAEDRRRLGLHGEVNFPGSGKKRKFPVRVPGVAPSVLFDLLLEW 60
DB 1 MODVGGPRPGSGDAEDRRRLGLHGEVNFPGSGKKRKFPVRVPGVAPSVLFDLLLEW 60

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QY 61 HLPAPNLVSLVGEOPFAMKSMRLDVLKGLVKAQSTGAMILTSALRVLARHVQAV 120
DB 61 HLPAPNLVSLVGEOPFAMKSMRLDVLKGLVKAQSTGAMILTSALRVLARHVQAV 120
QY 121 RHSLASTSKRVAVAGMASLGRVLRHRIIEBAQEDPVVHYPEDDGSQGLCSLDSVL 180
DB 121 RHSLASTSKRVAVAGMASLGRVLRHRIIEBAQEDPVVHYPEDDGSQGLCSLDSVL 180
QY 181 SHPIIIVPEPGKDGITELRLRLKXHSI SEORAGYGTSTIEIPVLCILVNDPNTLERI 240
DB 181 SHPIIIVPEPGKDGITELRLRLKXHSI SEORAGYGTSTIEIPVLCILVNDPNTLERI 240
QY 241 SBAVEAPAMWILVSGGIADVLALVNOPHLLVPEKVAEKORKEKPSKHFSEWIDIVRT 300
DB 241 SBAVEAPAMWILVSGGIADVLALVNOPHLLVPEKVAEKORKEKPSKHFSEWIDIVRT 300
QY 301 KLLQNTSHQHLLTYVDFEQSGSEELDTYLKALVKAQSHQEPQDYLDELKLVANDR 360
DB 301 KLLQNTSHQHLLTYVDFEQSGSEELDTYLKALVKAQSHQEPQDYLDELKLVANDR 360
QY 361 VIAKSEIFNGDVEMKSCDLEEVNDALVSNKPEFVRLFDNGADVADFLTYGRLQELVR 420
DB 361 VIAKSEIFNGDVEMKSCDLEEVNDALVSNKPEFVRLFDNGADVADFLTYGRLQELVR 420
QY 421 SVSRKSLLEFDLQKQEBARLTLAGLGTQAKREPAPPAFSLHEVSVLKDFLQDADCRG 480
DB 421 SVSRKSLLEFDLQKQEBARLTLAGLGTQAKREPAPPAFSLHEVSVLKDFLQDADCRG 480
QY 481 PVOQDGPGRRAAEKGRAPKPTGQKWLDLNOKSENPMWDLFLMAVLQNRHMAATYFMAM 540
DB 481 PVOQDGPGRRAAEKGRAPKPTGQKWLDLNOKSENPMWDLFLMAVLQNRHMAATYFMAM 540
QY 541 GQEGVAAALAAKIIKEMSHLETEBAARATREAKERLALPFSCEVNSBARAFALLV 600
DB 541 GQEGVAAALAAKIIKEMSHLETEBAARATREAKERLALPFSCEVNSBARAFALLV 600
QY 601 RNRNCKSKTTCCHLATEADAKAFPAHDVQVAFTRIWMGDMAAGTRIILLAGLFCFALV 660
DB 601 RNRNCKSKTTCCHLATEADAKAFPAHDVQVAFTRIWMGDMAAGTRIILLAGLFCFALV 660
QY 661 YNNLTTFSEAPLRGLDLDLSDLTEKSPLYGIQSRVEELVEAPRAQGRGRAVFL 720
DB 661 YNNLTTFSEAPLRGLDLDLSDLTEKSPLYGIQSRVEELVEAPRAQGRGRAVFL 720
QY 721 LTRMRKFMGAPVTVFIGNVVMFAFLFTYVLDVFRPPQSGSPBETLLYFWFTLV 780
DB 721 LTRMRKFMGAPVTVFIGNVVMFAFLFTYVLDVFRPPQSGSPBETLLYFWFTLV 780
QY 781 BEIRQGFPTDEDTLHVKFTLLYVGNMNCMDVAIFLPIVGTCTMLPSAFBAGRTVLAM 840
DB 781 BEIRQGFPTDEDTLHVKFTLLYVGNMNCMDVAIFLPIVGTCTMLPSAFBAGRTVLAM 840
QY 841 DPMVETLRLIHFALHKOIGPKIYVERMKCVFFFLFLSLVLAAYGTTQALLHPHDG 900
DB 841 DPMVETLRLIHFALHKOIGPKIYVERMKCVFFFLFLSLVLAAYGTTQALLHPHDG 900
QY 901 RLEWIFRRRLYRPIYOIFQIPLDEIDEARVNCSTPILLEDSPSCPSLYAMWLVITLLV 960
DB 901 RLEWIFRRRLYRPIYOIFQIPLDEIDEARVNCSTPILLEDSPSCPSLYAMWLVITLLV 960
QY 961 TELLVNTVNLMLLAFSFTYQVVGNAWMEKFORVNLIVEYHERPALAPFILLSHL 1020
DB 961 TELLVNTVNLMLLAFSFTYQVVGNAWMEKFORVNLIVEYHERPALAPFILLSHL 1020
QY 1021 SLTLRRVFEKKEAEHREHLERDLPDLQKVTWETVQENFLSYMEKRRDSEGBVLK 1080
DB 1021 SLTLRRVFEKKEAEHREHLERDLPDLQKVTWETVQENFLSYMEKRRDSEGBVLK 1080
QY 1081 TAAHVDLAKYVGLREBEKRIKCLESOJNVCVSVSSVADVLACGGGRSSOHGEGSQ 1140
DB 1081 TAAHVDLAKYVGLREBEKRIKCLESOJNVCVSVSSVADVLACGGGRSSOHGEGSQ 1140
QY 1141 LVAADHRGGLDGEOPGAGQPPSDT 1165

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DB 1141 LVAADHRGGLDGEOPGAGQPPSDT 1165
RESULT 2
AC Q9NY34 PRELIMINARY; PRT: 1159 AA.
ID Q9NY34;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE LTRPC5 protein (fragment).
GN LTRPC5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Paulsen M., El-Maarri O., Engemann S., Franck O., Stroedicke M.,
RA Davies K.R., Bowden L.M., Reinhardt R., Reik W., Harteneck C.,
RA Walter J.;
RT "Comparative sequence analysis and characterization of the imprinting
RT cluster on the human chromosome 11p15.5 and distal mouse chromosome
RT 7."
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ270996; CAB6342.1; -.
DR InterPro: IPR002111; Cat_channel_TripL.
DR InterPro: IPR005821; Ion_trans.
DR Pfam: PF00520; Ion_trans.
DR Ionic channel; Transmembrane.
FT NON-TER
SQ SEQUENCE 1159 AA; 130775 MW; E31658C1125363B CRC64;
Query Match 98.8%; Score 6019; DB 4; Length 1159;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1154; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
QY 9 PSPPDADRRRELGLHREGVNFGGKRGKGFVRPVSVAASVLPDILLAEHMLPAPMLV 68
DB 1 PSPPDADRRRELGLHREGVNFGGKRGKGFVRPVSVAASVLPDILLAEHMLPAPMLV 68
QY 69 VSLVGEOPFAMKSMRLDVLKGLVKAQSTGAMILTSALRVLARHVQAVRHSLAST 128
DB 69 VSLVGEOPFAMKSMRLDVLKGLVKAQSTGAMILTSALRVLARHVQAVRHSLAST 128
QY 129 STKRVAVAGMASLGRVLRHRIIEBAQ--EDPPHYPPEDDGSQGLCSLDSNLSHFTLV 186
DB 129 STKRVAVAGMASLGRVLRHRIIEBAQ--EDPPHYPPEDDGSQGLCSLDSNLSHFTLV 186
QY 187 EPGPGKGDGTELRLRLKXHSI SEORAGYGTSTIEIPVLCILVNDPNTLERISRAVEO 246
DB 187 EPGPGKGDGTELRLRLKXHSI SEORAGYGTSTIEIPVLCILVNDPNTLERISRAVEO 246
QY 247 AAPMLIIVSGGIADVLALVNOPHLLVPEKVAEKORKEKPSKHFSEWIDIVRTKLLONI 306
DB 247 AAPMLIIVSGGIADVLALVNOPHLLVPEKVAEKORKEKPSKHFSEWIDIVRTKLLONI 306
QY 307 TSHQHLTVYVPEPGSGSEELDTYLKALVKAQSHQEPQDYLDELKLVANDRVDIAKS 366
DB 307 TSHQHLTVYVPEPGSGSEELDTYLKALVKAQSHQEPQDYLDELKLVANDRVDIAKS 366
QY 367 EIPFNDVEMKSCDLEEVNDALVSNKPEFVRLFDNGADVADFLTYGRLQELYRSVSRKS 426
DB 367 EIPFNDVEMKSCDLEEVNDALVSNKPEFVRLFDNGADVADFLTYGRLQELYRSVSRKS 426
QY 427 LFLDLQKQEBARLTLAGLGTQAKREPAPPAFSLHEVSVLKDFLQDADCRGYODGR 486
DB 427 LFLDLQKQEBARLTLAGLGTQAKREPAPPAFSLHEVSVLKDFLQDADCRGYODGR 486
QY 487 PGRRRRAEKGAPKPTGQKWLDLNOKSENPMWDLFLMAVLQNRHMAATYFMAMQOEGVA 546
DB 487 PGRRRRAEKGAPKPTGQKWLDLNOKSENPMWDLFLMAVLQNRHMAATYFMAMQOEGVA 546

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QY 547 AALAACTLKEMSHUETEAARATREAKYERLALDLFSECCYSNSEARAFAALLVRRNCW 606
 Db 541 AALAACTLKEMSHUETEAARATREAKYERLALDLFSECCYSNSEARAFAALLVRRNCW 600
 QY 607 SKTCTLHATENDADAFPAHDGVQAFLTRIMWGDMAAGTPILRLGAFCLCPALVYTNLTIT 666
 Db 601 SKTCTLHATENDADAFPAHDGVQAFLTRIMWGDMAAGTPILRLGAFCLCPALVYTNLTIT 660
 QY 667 FSEAPLRTGLEDDLODLSLDTREKSPYLGLGSRVEELVEAPRAQDGRGPAFELLTRMRK 726
 Db 661 FSEAPLRTGLEDDLODLSLDTREKSPYLGLGSRVEELVEAPRAQDGRGPAFELLTRMRK 720
 QY 727 FWGAPVTVFLGNVWYFAFLFLFTYVLLVDFRPPQSGSGPEVTLTFWVFTLVLEIRIG 786
 Db 721 FWGAPVTVFLGNVWYFAFLFLFTYVLLVDFRPPQSGSGPEVTLTFWVFTLVLEIRIG 780
 QY 787 FTTDEDTLHVKKFTLYVGDNNKCMVAIFLFTVGTCTMLPSAEAGRTVLAMDPMVFT 846
 Db 781 FTTDEDTLHVKKFTLYVGDNNKCMVAIFLFTVGTCTMLPSAEAGRTVLAMDPMVFT 840
 QY 847 LRLHIIPAIHKOLGPKITIVERMMKDVFFPLFELSVMIVAVGVTQALLHPHDSLEWIF 906
 Db 841 LRLHIIPAIHKOLGPKITIVERMMKDVFFPLFELSVMIVAVGVTQALLHPHDSLEWIF 900
 QY 907 RRVLYRPYLOIFGQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANMLVILLVFLVLT 966
 Db 901 RRVLYRPYLOIFGQIPLDEIDEARVNCSTHPLLEDSPSCPSLYANMLVILLVFLVLT 960
 QY 967 NVLLMNLIIAMSYTFQVVOGNATPMKFORNYLIVEYHERPALAPPTILSHSLTTR 1026
 Db 961 NVLLMNLIIAMSYTFQVVOGNATPMKFORNYLIVEYHERPALAPPTILSHSLTTR 1020
 QY 1027 VFKEAEKREHLEBDLPDQKVVYVETVOKENFLSKMEKRDRSGEVLRKTAHVD 1086
 Db 1021 VFKEAEKREHLEBDLPDQKVVYVETVOKENFLSKMEKRDRSGEVLRKTAHVD 1080
 QY 1087 FIAKTLGLRBOEKIKCLSEQINYSVLSVADVLAAQGGPRSSQHCGESSQIYAADH 1146
 Db 1081 FIAKTLGLRBOEKIKCLSEQINYSVLSVADVLAAQGGPRSSQHCGESSQIYAADH 1140
 QY 1147 RGGIDGWEQPGAGPPSDT 1165
 Db 1141 RGGIDGWEQPGAGPPSDT 1159

RESULT 3

Q9JUH7 PRELIMINARY; PRT; 1158 AA.

AC Q9JUH7; 01-OCT-2000 (Tremblrel. 15, Created)

DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)

DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)

DE MSLN1-and TRP-related protein 1 (MTR1).

GN TRPM5 OR LTRP5 OR MTR1.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxId=10990;

RA NCI Sequence from N.A.

RA yacutk H., Watanabe H., Hattori M., Joh K., Soejima H., Komoda H., Xie Z., Zhu X., Higashimoto K., Nishimura M., Kuratomi S., Sasaki H., Sasaki Y., Maki T.

RT "Sequence-based structural features between Kv1q1 and Tapal on mouse chromosome 7q4/f5 corresponding to the Beckwith-Wiedemann syndrome intronic sequences of Kv1q1 between mouse and human.";

RT DNA Res. 7:195-206(2000).

RP SEQUENCE FROM N.A.

RX MEDLINE=2036135; PubMed=10903843;

RA Enklaar T., Esswein M., Oswald M., Hilbert K., Winterpacht A., Higgins M., Zabel B., Prawitt D., "Mtr1, a Novel Ballelically Expressed Gene in the Center of the Mouse Distal Chromosome 7 Imprinting Cluster, is a Member of the Trp Gene Family," Genomics 67:179-187(2000).

DR EMBL: AB039952; BAA96877.1; -

DR EMBL: AF228681; AAF98120.1; -

DR MGI: 1861718; Trpm5.

DR InterPro: IPR002111; Cat_channel_TrpL.

DR InterPro: IPR005821; Ion_trans.

DR Pfam: PF00520; Ion_trans; 1.

KW Ionc channel; Transmembrane.

SEQUENCE 1158 AA; 130843 MW; FOA5237EC67867CE CRC64;

Query Match 83.2%; Score 5068.5; DB 11; Length 1158; Best Local Similarity 83.9%; Pred. No. 0; Matches 980; Conservative 66; Mismatches 109; Indels 13; Gaps 4;

QY 1 MODVQPPGSPGADREDELGRGEVNFSGSKGKGFVYRPSGVAPSVLFDLLAEW 60

Db 1 MOTTQSGCGSPPTDECMEPILCRGEINFGSGKKGKGFVYRPSGVAPSVLFDLLAEW 60

QY 61 HLPAPNLVSLVGERPLAMKSWLRDVLKGLVYAAQSTGAMILTSALRVGLARRVQAV 120

Db 61 HLPAPNLVSLVGERPLAMKSWLRDVLKGLVYAAQSTGAMILTSALRVGLARRVQAV 120

QY 121 RDHSLASTSTVRYVAVGMAISGLVLRRLIE--EAQEDFVYHPEDEGSGGPGICSDS 178

Db 121 RDHSLASTSTKIRVAVAGMALDRIHRLQLLDGVHOKEDTPIHPADGNTQGPLCPIDS 180

QY 179 NLSHFLVPEPPPKG--DGLTELRLLEKHSIEQAGVGGSIPIPLCLLVNDDPTL 237

Db 181 NLSHFLVPEPPPKG--DGLTELRLLEKHSIEQAGVGGSIPIPLCLLVNDDPTL 240

QY 238 ERISRAVEQAAPWILVSGGSIADVLAAVQNPPLVLPKVAEKQFEKFPKHSWEDIV 297

Db 241 ERISRAVEQAAPWILVSGGSIADVLAAVQNPPLVLPKVAEKQFEKFPKHSWEDIV 300

QY 298 RWTLLQNTHTSHOHLTYVDEQSGSELDVILKALVYKAKSHSQEODYLDLKLAVA 357

Db 301 RWTLLQNTHTSHOHLTYVDEQSGSELDVILKALVYKAKSHSQEODYLDLKLAVA 360

QY 358 WDRVDIAKSEIFNGDVWKSCLDEWVVDALVSNKPEFVRLFYVNGADVADFLYGRLOE 417

Db 361 WDRVDIAKSEIFNGDVWKSCLDEWVVDALVSNKPEFVRLFYVNGADVADFLYGRLOE 420

QY 418 LYRSVSRKSLFDLLQKQEARLTLAAGTQARBPAPAPAFSLHESRVLDLFLDA 477

Db 421 LYRSVSRKSLFDLLQKQEARLTLAAGTQARBPAPAPAFSLHESRVLDLFLDA 480

QY 478 CRGYQDGRPEDRRRAEKPAKRTGQKWLIDLNQKSENPVRDILPLAVLONRHMATYF 537

Db 481 CRGYQDGRPEDRRRAEKPAKRTGQKWLIDLNQKSENPVRDILPLAVLONRHMATYF 536

QY 538 WAMGQGVAAALAACTLKEMSHUETEAARATREAKYERLALDLFSECCYSNSEARAFA 597

Db 537 WAMGQGVAAALAACTLKEMSHUETEAARATREAKYERLALDLFSECCYSNSEARAFA 596

QY 598 LTVRRNCSKTTCTLHATENDADAFPAHDGVQAFLTRIMWGDMAAGTPILRLGAFCLCF 657

Db 597 LTVRRNCSKTTCTLHATENDADAFPAHDGVQAFLTRIMWGDMAAGTPILRLGAFCLCF 656

QY 658 ALVYTNLTITSEEPALRTGLEDDLODLSLDTREKSPYLGLGSRVEELVEAPRAQDGRGPA 717

Db 657 ALVYTNLTITSEEPALRTGLEDDLODLSLDTREKSPYLGLGSRVEELVEAPRAQDGRGPA 716

QY 718 VFLLTRRKFWGAVTVFLGNVWYFAFLFLFTYVLLVDFRPPQSGSGPEVTLTFWVFT 777

Db 717 VFLLTRRKFWGAVTVFLGNVWYFAFLFLFTYVLLVDFRPPQSGSGPEVTLTFWVFT 776

QY 778 LVLEIRIQGFTEDTLHVKKFTLYVGDNNKCMVAIFLFTVGTCTMLPSAEAGRTV 837

Db 777 LVLEIRIOGFPTDEBTHLVKKFTLVYEDNMNKCDAVAFILFVGVTCRMVPSVFEAGRTV 836
 Qy 838 LAMDMVFTLRILHFAHKOGLGPKIIVERMKAVFPFLFSLVWLVAYGTTQALLHP 897
 Db 837 LAIDMVFTRLIHFALHKOGLGPKIIVERMKAVFPFLFSLVWLVAYGTTQALLHP 896
 Qy 898 HDGRLEWIFRRVLYRPLYQIFQOIPLDEIDEARVNCSTHPLLEDSPCSPSLYANWLVL 957
 Db 897 HDGRLEWIFRRVLYRPLYQIFQOIPLDEIDEARVNCSTHPLLEDSPCSPSLYANWLVL 956
 Qy 958 LVLFTLVNTVNLMLLIAMFSYTFQVVGQNAFMWKFQRYNLIVEYHERPALAPFILL 1017
 Db 957 LVLFTLVNTVNLMLLIAMFSYTFQVVGQNAFMWKFQRYNLIVEYHERPALAPFILL 1016
 Qy 1018 SHLSLTLRVFKKEHKEHREHRLPDLQKVTWETVQKENTLSKMEKRRRDSGEV 1077
 Db 1017 SHLSLTLRVFKKEHKEHREHRLPDLQKVTWETVQKENTLSKMEKRRRDSGEV 1076
 Qy 1078 LKRTAHRVDLAKYIGGLREOEKRIKLESQINYSVLVSVADYLAOGGPRSSQHCSE 1137
 Db 1077 LKRTAHRVDLAKYIGGLREOEKRIKLESQINYSVLVSVADYLAOGGPRSSQHCSE 1136
 Qy 1138 GSQLVADHRRGIDGMEQPGACQPPSDT 1165
 Db 1137 RSQPASARDR-----EYLESGLPPSDT 1158

RESULT 4

Q9EBM4 PRELIMINARY; PRT; 1148 AA.
 ID Q9EBM4: 01-MAR-2001 (TREMBlrel. 16, Created)
 AC Q9EBM4: 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE ltrpc5 protein.
 GN TRPM5 OR LTRPC5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX SEQUENCE FROM N.A.
 RC STRAIN=129 SV;
 RA MEDLINE=20377495; PubMed=10915772;
 RA Paulsen M., El-Maarti O., Engemann S., Stroedicke M., Franck O.,
 RA Davies K., Reinhardt R., Reik W., Walter J.;
 RA "Sequence conservation and variability of imprinting in the Beckwith-
 RT Wiedemann syndrome gene cluster in human and mouse.";
 RT Hum. Mol. Genet. 9:1829-1841(2000).
 DR EMBL; AJ251835; CAC19456.1; -
 DR MGD; MGI:1861718; Trpm5.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_trans.
 DR Pfam; PF00520; Ion_trans.1.
 KM Ionic channel; Transmembrane.
 SQ SEQUENCE 1148 AA; 129630 MW; 947AF5B9CFDCA127 CRC64;

Query Match 82.4%; Score 5018.5; DB 11; Length 1148;
 Best Local Similarity 85.3%; Pred. No. 0;
 Matches 964; Conservative 63; Mismatches 96; Indels 7; Gaps 3;

Qy 1 MODVCGPRGSGDADREELGHRGEVNFSGGKRGKRVNPSVAPSVFDILLAEW 60
 Db 1 MOTTGSSCGSPEDTDEGWEPLCRGEINFGSGGKRGKRVNPSVAPSVFDILLAEW 60
 Qy 61 HLPAPLVVSLVGEOPFAMKSWLRDYLKRGGLVKAQSTGAMITLSALRGLARHVGAV 120
 Db 61 HLPAPLVVSLVGEOPFAMKSWLRDYLKRGGLVKAQSTGAMITLSALRGLARHVGAV 120
 Qy 121 RDSHSLASTSTKRVVAVNAGSLGRVLAHRLLE--EAQEDFPVHYPEDDGSGGQPLCSLDS 178
 Db 121 RDSHSLASTSTKRVVAVNAGSLGRVLAHRLLE--EAQEDFPVHYPEDDGSGGQPLCSLDS 180

Qy 179 NLSHFILVEPGPCKG-DGLTELRRLRLEKHSIQEAGYGTGSIPIVLCLLVNGDPNTL 237
 Db 181 NLSHFILVESGALSGNDGLTELQSLSEKHSIQEAGYGTGSIPIVLCLLVNGDPNTL 240
 Qy 238 ERISRAVEQAAPMLILVSGGIGADYLAALVNQPHLVKVAEKEQFKEKFPSEKHSMEIV 297
 Db 241 ERISRAVEQAAPMLILVSGGIGADYLAALVNQPHLVKVAEKEQFKEKFPSEKHSMEIV 300
 Qy 298 RMTKLQNTSHOHLITVYDEQSGSELDIVILKALVKAKCSHQEQDYLDELKLAVA 357
 Db 301 HMTLQNTIAHPHLLITVYDEQSGSELDIVILKALVKAKCSHQEQDYLDELKLAVA 360
 Qy 358 WDRVDIAKSEIFNGDVEKSCDLEEVNVDALVSNKPEFVRLFVNDGADVADFLTYGRLOE 417
 Db 361 WDRVDIAKSEIFNGDVEKSCDLEEVNVDALVSNKPEFVRLFVNDGADVADFLTYGRLOE 420
 Qy 418 LYRSYRSKSLFDLQROEABRLTLAQLGVOARERPPAGSPASLHVSVLXDFLQDA 477
 Db 421 LYHSVSPKSLFELLQRGHEGRLLTAGLGAQAARELP1GLPASFHVSRLKDFLHDA 480
 Qy 478 CRGFYQDGRPGDRBRAEKPAKRPFGQKMLDLNOKSENPMRDLFLMAVLQNRHEMATYF 537
 Db 481 CRGFYQDG---RMEERGPFRKRPAGQKMLDLNOKSENPMRDLFLMAVLQNRHEMATYF 536
 Qy 538 WAMGQEGVAAALAAACKLIKEMSHLETEAARATREARYERLADLFSECYSNSERAPFA 597
 Db 537 WAMGREGVAAALAAACKLIKEMSHLETEAARATREARYERLADLFSECYSNSERAPFA 596
 Qy 598 LTVRRNRCSKTTCLHATEADAKAFPHDGVQAFRTIWMGDMAAGTPIRLILGAPLCF 657
 Db 597 LTVRRNRCSKTTCLHATEADAKAFPHDGVQAFRTIWMGDMAAGTPIRLILGAPLCF 656
 Qy 658 ALVTNLTFSBEAPLRTGLDLDLDTKEPSFLYGLOSREVELEAPRAQGRGPRA 717
 Db 657 ALVTNLTFSBEAPLRTGLDLDLDTKEPSFLYGLOSREVELEAPRAQGRGPRA 716
 Qy 718 VFLTRMRKFWGAPVTFVGNVVFAPLFLFTYVLLVDFRPPGSGPEVTLYFWVFT 777
 Db 717 AFLTRMRKFWGAPVTFVGNVVFAPLFLFTYVLLVDFRPPGSGPEVTLYFWVFT 776
 Qy 778 LVLEIRIOGFPTDEBTHLVKKFTLVYEDNMNKCDAVAFILFVGVTCRMVPSVFEAGRTV 837
 Db 777 LVLEIRIOGFPTDEBTHLVKKFTLVYEDNMNKCDAVAFILFVGVTCRMVPSVFEAGRTV 836
 Qy 838 LAMDMVFTLRILHFAHKOGLGPKIIVERMKAVFPFLFSLVWLVAYGTTQALLHP 897
 Db 837 LAIDMVFTRLIHFALHKOGLGPKIIVERMKAVFPFLFSLVWLVAYGTTQALLHP 896
 Qy 898 HDGRLEWIFRRVLYRPLYQIFQOIPLDEIDEARVNCSTHPLLEDSPCSPSLYANWLVL 957
 Db 897 HDGRLEWIFRRVLYRPLYQIFQOIPLDEIDEARVNCSTHPLLEDSPCSPSLYANWLVL 956
 Qy 958 LVLFTLVNTVNLMLLIAMFSYTFQVVGQNAFMWKFQRYNLIVEYHERPALAPFILL 1017
 Db 957 LVLFTLVNTVNLMLLIAMFSYTFQVVGQNAFMWKFQRYNLIVEYHERPALAPFILL 1016
 Qy 1018 SHLSLTLRVFKKEHKEHREHRLPDLQKVTWETVQKENTLSKMEKRRRDSGEV 1077
 Db 1017 SHLSLTLRVFKKEHKEHREHRLPDLQKVTWETVQKENTLSKMEKRRRDSGEV 1076
 Qy 1078 LKRTAHRVDLAKYIGGLREOEKRIKLESQINYSVLVSVADYLAOGG 1127
 Db 1077 LKRTAHRVDLAKYIGGLREOEKRIKLESQINYSVLVSVADYLAOGG 1126

RESULT 5
 Q99NF9 PRELIMINARY; PRT; 1148 AA.
 ID Q99NF9: 01-JUN-2001 (TREMBlrel. 17, Created)
 AC Q99NF9: 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE ltrpc5 protein.

Qy 1078 LKRTAHRVDLAKYIGGLREOEKRIKLESQINYSVLVSVADYLAOGG 1127
 Db 1077 LKRTAHRVDLAKYIGGLREOEKRIKLESQINYSVLVSVADYLAOGG 1126

GN TRPM5 OR LTRPC5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=129 SV;
 RA Stroedicke M.;
 RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129 SV;
 RX MEDLINE=20377495; PubMed=10915772;
 RA Paulsen M., El-Maazri O., Engemann S., Stroedicke M., Franck O.,
 RA Davies K., Reinhardt R., Reik W., Walter J.;
 RT "Sequence conservation and variability of imprinting in the Beckwith-
 RT Wiedemann syndrome gene cluster in human and mouse.";
 RL Hum. Mol. Genet. 9:1829-1841(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129 SV;
 RC STRAIN=129 SV;
 RA Engemann S.;
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AJ271092; CAB94717.2; --
 DR MGD; MGI:1861718; Trpm5.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_channel_TrpL.
 DR Pfam; PF00520; Ion_trans_1.
 KM Ionic channel; Transmembrane.
 SQ SEQUENCE 1148 AA; 129590 MW; 90517E8557DCA127 CRC64;
 Query Match 82.2%; Score 5008.5; DB 11; Length 1148;
 Best Local Similarity 85.2%; Pred. No. 0;
 Matches 963; Conservative 63; Mismatches 97; Indels 7; Gaps 3;

QY 1 MGVVQGPSPGDAEDRELGLHGEVNFSGSGKRGKRVVPSPGAVSVLPDILLAEW 60
 DB 1 MGVVQGPSPGDAEDRELGLHGEVNFSGSGKRGKRVVPSPGAVSVLPDILLAEW 60
 QY 61 HLPAPNLVSVLGEQPPAMKSWLRDVLRKLVKAACTGAWILTSARVGLARVGVAV 120
 DB 61 HLPAPNLVSVLGEQPPAMKSWLRDVLRKLVKAACTGAWILTSARVGLARVGVAV 120
 QY 121 RDHSLASTSTKYVAVVAGMASLGRVLRHRIE--EAQDPFVHYEDDDGSGGSLPCLSDS 178
 DB 121 RDHSLASTSTKYVAVVAGMASLGRVLRHRIE--EAQDPFVHYEDDDGSGGSLPCLSDS 178
 QY 121 RDHSLASTSTKYVAVVAGMASLGRVLRHRIE--EAQDPFVHYEDDDGSGGSLPCLSDS 180
 DB 121 RDHSLASTSTKYVAVVAGMASLGRVLRHRIE--EAQDPFVHYEDDDGSGGSLPCLSDS 180
 QY 179 NLSHFILVEPGPPGKG-DGLTELRLRLKHI SEQRAVGGTSGIEIPVLCILVNGDPNTL 237
 DB 179 NLSHFILVEPGPPGKG-DGLTELRLRLKHI SEQRAVGGTSGIEIPVLCILVNGDPNTL 237
 QY 181 NLSHFILVESGALSGNDGLTELQSLSEKHSIQRTGYGTSICIQIPVLCILVNGDPNTL 240
 DB 181 NLSHFILVESGALSGNDGLTELQSLSEKHSIQRTGYGTSICIQIPVLCILVNGDPNTL 240
 QY 238 ERIRAVEQAPWILLVSSGGIADVLALVNQPHLVKVAEKQPKKFKSHSMEIV 297
 DB 238 ERIRAVEQAPWILLVSSGGIADVLALVNQPHLVKVAEKQPKKFKSHSMEIV 297
 QY 241 ERIRAVEQAPWILLVSSGGIADVLALVNQPHLVKVAEKQPKKFKSHSMEIV 300
 DB 241 ERIRAVEQAPWILLVSSGGIADVLALVNQPHLVKVAEKQPKKFKSHSMEIV 300
 QY 298 RWTKLQNTSHQHLTYDFEEOGSEBELDVIYIKALKVAKCKSHQSOEDYLDELKLAVA 357
 DB 298 RWTKLQNTSHQHLTYDFEEOGSEBELDVIYIKALKVAKCKSHQSOEDYLDELKLAVA 357
 QY 301 HMTLQNTIAHPHLTYDFEEOGSEBELDVIYIKALKVAKCKSHQSOEDYLDELKLAVA 360
 DB 301 HMTLQNTIAHPHLTYDFEEOGSEBELDVIYIKALKVAKCKSHQSOEDYLDELKLAVA 360
 QY 358 WDRVDIAKSEIFNGDVWKSCLDEEVVADLVSNKPEFVRLFVNDGADVADFLTYGRLOE 417
 DB 358 WDRVDIAKSEIFNGDVWKSCLDEEVVADLVSNKPEFVRLFVNDGADVADFLTYGRLOE 417
 QY 361 WDRVDIAKSEIFNGDVWKSCLDEEVVADLVSNKPEFVRLFVNDGADVADFLTYGRLOE 420
 DB 361 WDRVDIAKSEIFNGDVWKSCLDEEVVADLVSNKPEFVRLFVNDGADVADFLTYGRLOE 420
 QY 418 LYRSVSRKSLFDLLQKQEBARLTLAGLGTQQAAREPAPGAPPAHVSRLKDFLODA 477
 DB 418 LYRSVSRKSLFDLLQKQEBARLTLAGLGTQQAAREPAPGAPPAHVSRLKDFLODA 477
 QY 421 LYHSVSPSLLFELLQKQEBARLTLAGLGTQQAAREPAPGAPPAHVSRLKDFLODA 480
 DB 421 LYHSVSPSLLFELLQKQEBARLTLAGLGTQQAAREPAPGAPPAHVSRLKDFLODA 480
 QY 478 CRGYQDGRPGDRAAEKPAKPTGQKWLNDLNKSENPRDPLFMAVILNBRHEMATYF 537
 DB 478 CRGYQDGRPGDRAAEKPAKPTGQKWLNDLNKSENPRDPLFMAVILNBRHEMATYF 537
 QY 481 CRGYQDGRPGDRAAEKPAKPTGQKWLNDLNKSENPRDPLFMAVILNBRHEMATYF 536
 DB 481 CRGYQDGRPGDRAAEKPAKPTGQKWLNDLNKSENPRDPLFMAVILNBRHEMATYF 536
 QY 538 WAMQEGVAAALAAACKILKEMSHLETEAARATREAKYERLADLFSECYNSBARAFA 597
 DB 538 WAMQEGVAAALAAACKILKEMSHLETEAARATREAKYERLADLFSECYNSBARAFA 597

DB 537 WAMQEGVAAALAAACKILKEMSHLETEAARATREAKYERLADLFSECYNSBARAFA 596
 QY 598 LTVRRNCSWSTTGLAHATEADAKAFPHQDVQAFTRIRIMGDMAGPILRLGALFCF 657
 DB 597 LTVRRNCSWSTTGLAHATEADAKAFPHQDVQAFTRIRIMGDMAGPILRLGALFCF 656
 QY 658 ALVYTNLITFSEEAFLRTGLEDLQDLSDTEKSPLYLGQSRVEELVEAPAPQDGRGPA 717
 DB 657 ALVYTNLITFSEEAFLRTGLEDLQDLSDTEKSPLYLGQSRVEELVEAPAPQDGRGPA 716
 QY 717 VELLTRMRKFWGAVTVFLGNVVMYFAFLFTYVLLVDFRPPQSGSPGSEVTLTFVWFT 777
 DB 717 VELLTRMRKFWGAVTVFLGNVVMYFAFLFTYVLLVDFRPPQSGSPGSEVTLTFVWFT 776
 QY 778 LVEEIQGFPTDDTHLYKKEFTLYVGDNNKCMVAFPLFTVGTQRMPLPSAEAGRTV 837
 DB 777 LVEEIQGFPTDDTHLYKKEFTLYVGDNNKCMVAFPLFTVGTQRMPLPSAEAGRTV 836
 QY 838 LAMPVFTLRLIHPAHLKQGPRIIVERMRKDVFFFLPFLSVMLVAVGTTQALLHP 897
 DB 837 LAMPVFTLRLIHPAHLKQGPRIIVERMRKDVFFFLPFLSVMLVAVGTTQALLHP 896
 QY 898 HDGRLWIFRRVLYRPLYQIFGQIPLDEIDBARVNCSTHPLLEDSPGSLYANWVIL 957
 DB 897 HDGRLWIFRRVLYRPLYQIFGQIPLDEIDBARVNCSTHPLLEDSPGSLYANWVIL 956
 QY 958 LLYVFLVTVNLVNLNLIIMASYTFQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1017
 DB 957 LLYVFLVTVNLVNLNLIIMASYTFQVQVQVQVQVQVQVQVQVQVQVQVQVQV 1016
 QY 1018 SHLSLTVRVEKAEHREHLERDLPDLPQKVVTVETQKFNFLSMKRRRDSGEV 1077
 DB 1017 SHLSLTVRVEKAEHREHLERDLPDLPQKVVTVETQKFNFLSMKRRRDSGEV 1076
 QY 1078 LKRTAHRVDIYAKYLGUREQEKIKCLESGQINYSVAVSSVADVLAAQGG 1127
 DB 1077 LKRTAHRVDIYAKYLGUREQEKIKCLESGQINYSVAVSSVADVLAAQGG 1126

RESULT 6
 Q9EPM3 PRELIMINARY; PRT; 1116 AA.
 ID Q9EPM3
 AC Q9EPM3
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
 DE Ltrpc5 protein.
 GN TRPM5 OR LTRPC5.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129 SV;
 RX MEDLINE=20377495; PubMed=10915772;
 RA Paulsen M., El-Maazri O., Engemann S., Stroedicke M., Franck O.,
 RA Davies K., Reinhardt R., Reik W., Walter J.;
 RT "Sequence conservation and variability of imprinting in the Beckwith-
 RT Wiedemann syndrome gene cluster in human and mouse.";
 RL Hum. Mol. Genet. 9:1829-1841(2000).
 DR EMBL; AJ251835; CAC19457.1; --
 DR MGD; MGI:1861718; Trpm5.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR005821; Ion_channel_TrpL.
 DR Pfam; PF00520; Ion_trans_1.
 KM Ionic channel; Transmembrane.
 SQ SEQUENCE 1116 AA; 126608 MW; 32DFA8CF2835E48 CRC64;

Query Match 81.5%; Score 4963.5; DB 11; Length 1116;
 Best Local Similarity 85.6%; Pred. No. 0;
 Matches 954; Conservative 60; Mismatches 93; Indels 7; Gaps 3;

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QY 1 MODVCGRRPGSGDAEDRRELGLHREGEVNGGGGKKRGKFEVAVPSGVAPSVLFDLLLEW 60
Db 1 MOTTSSCGSPPTDEDEGWEPLCRGEINFGSGGKRGKFEVAVPSGVAPSVLFDLLLEW 60
QY 61 HLPAPNLVSLVGEBOFPAMKSMRLDVLKGLVKAAOSTGAMILTSALRVGLARHVQAV 120
Db 61 HLPAPNLVSLVGEBOFPAMKSMRLDVLKGLVKAAOSTGAMILTSALRVGLARHVQAV 120
QY 121 RDHSLASTSTKVRVAVAGMAGSLGRVLRHRLT--EAQEDFPVHYBEDDGGSGPLCSLDS 178
Db 121 RDHSLASTSTKVRVAVAGMAGSLGRVLRHRLT--EAQEDFPVHYBEDDGGSGPLCSLDS 178
QY 179 NLSHFLVSGALGSGNDGLTQSLERKHSIQOKRTGTCISQIPVCLLVNGDPNTL 240
Db 179 NLSHFLVSGALGSGNDGLTQSLERKHSIQOKRTGTCISQIPVCLLVNGDPNTL 240
QY 238 ERISSRAVEQAAPMLILVSGGIADVLAAALVNPQPHLLVPKVAEKQEPKSPKHSFWMEDIV 297
Db 238 ERISSRAVEQAAPMLILVSGGIADVLAAALVNPQPHLLVPKVAEKQEPKSPKHSFWMEDIV 297
QY 241 ERISSRAVEQAAPMLILVSGGIADVLAAALVNPQPHLLVPKVAEKQEPKSPKHSFWMEDIV 300
Db 241 ERISSRAVEQAAPMLILVSGGIADVLAAALVNPQPHLLVPKVAEKQEPKSPKHSFWMEDIV 300
QY 298 RMTKLLQNTSHOHLITVDFEBOGSEELDTYILKALVYACSHSGSEPDYIDELKLA 357
Db 298 RMTKLLQNTSHOHLITVDFEBOGSEELDTYILKALVYACSHSGSEPDYIDELKLA 357
QY 301 HMTTELLQNTAHAPHLITVDFEBOGSEELDTYILKALVYACSHSGSEADYIDELKLA 360
Db 301 HMTTELLQNTAHAPHLITVDFEBOGSEELDTYILKALVYACSHSGSEADYIDELKLA 360
QY 358 MWRVDIAKSEIFNGDVEWKSCLDEEVMVDALVSNKPEFRLFPVNDGADVADELTYGRLOE 417
Db 358 MWRVDIAKSEIFNGDVEWKSCLDEEVMVDALVSNKPEFRLFPVNDGADVADELTYGRLOE 417
QY 361 MWRVDIAKSEIFNGDVEWKSCLDEEVMVDALVSNKPEFRLFPVNDGADVADELTYGRLOE 420
Db 361 MWRVDIAKSEIFNGDVEWKSCLDEEVMVDALVSNKPEFRLFPVNDGADVADELTYGRLOE 420
QY 418 LYRSVSRKSLFDLQROKQEBARLTLAGLGTQOAREPPVAPAFSLHESRVYLQFLODA 477
Db 418 LYRSVSRKSLFDLQROKQEBARLTLAGLGTQOAREPPVAPAFSLHESRVYLQFLODA 477
QY 421 LVHSVSKLFDLQROKQEBARLTLAGLGTQOAREPPVAPAFSLHESRVYLQFLODA 480
Db 421 LVHSVSKLFDLQROKQEBARLTLAGLGTQOAREPPVAPAFSLHESRVYLQFLODA 480
QY 478 CRGFYODGRRRAEKGPAPKPTGQKWLILNQSENPRDLFLMANVLQNRHEMATTF 537
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QY 481 CRGFYODGRRRAEKGPAPKPTGQKWLILNQSENPRDLFLMANVLQNRHEMATTF 536
Db 481 CRGFYODGRRRAEKGPAPKPTGQKWLILNQSENPRDLFLMANVLQNRHEMATTF 536
QY 538 NMGOGGVAALAAACILKEMSHLETAEARAAREAKYERLALDFSECYSENSEARA 597
Db 538 NMGOGGVAALAAACILKEMSHLETAEARAAREAKYERLALDFSECYSENSEARA 597
QY 537 NMGOGGVAALAAACILKEMSHLETAEARAAREAKYERLALDFSECYSENSEARA 596
Db 537 NMGOGGVAALAAACILKEMSHLETAEARAAREAKYERLALDFSECYSENSEARA 596
QY 598 LVRNRKCSKTCTCLHATEADAKAFADGVQAFLTRIWMGDMAATPILRLGLAFLC 657
Db 598 LVRNRKCSKTCTCLHATEADAKAFADGVQAFLTRIWMGDMAATPILRLGLAFLC 657
QY 597 LVRNRKCSKTCTCLHATEADAKAFADGVQAFLTRIWMGDMAATPILRLGLAFLC 656
Db 597 LVRNRKCSKTCTCLHATEADAKAFADGVQAFLTRIWMGDMAATPILRLGLAFLC 656
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QY 657 ALVYTNLITFSEAPRTGLEDLQDLSLDTESPLVGLQSRVEELVEAPRAQDGPRA 716
Db 657 ALVYTNLITFSEAPRTGLEDLQDLSLDTESPLVGLQSRVEELVEAPRAQDGPRA 716
QY 718 VFLTRMRKMGAPVTVPLGNVVMYFAFLFTYVLLVDRPPPOGSGSEVTLVFMVFT 777
Db 718 VFLTRMRKMGAPVTVPLGNVVMYFAFLFTYVLLVDRPPPOGSGSEVTLVFMVFT 776
QY 717 APLTRMRKMGAPVTVPLGNVVMYFAFLFTYVLLVDRPPPOGSGSEVTLVFMVFT 776
Db 717 APLTRMRKMGAPVTVPLGNVVMYFAFLFTYVLLVDRPPPOGSGSEVTLVFMVFT 776
QY 778 LVLEIRQGFTEDETHLVKFFTLVYGDMMNKCDAVAFLEIVGTCRMLPSAFAEGRV 837
Db 778 LVLEIRQGFTEDETHLVKFFTLVYGDMMNKCDAVAFLEIVGTCRMLPSAFAEGRV 836
QY 777 LVLEIRQGFTEDETHLVKFFTLVYGDMMNKCDAVAFLEIVGTCRMLPSAFAEGRV 836
Db 777 LVLEIRQGFTEDETHLVKFFTLVYGDMMNKCDAVAFLEIVGTCRMLPSAFAEGRV 836
QY 838 LANDFVFTLRLLHIAIKQLCPKIIIVERRMKOVFFFLFETISWLVAVGTTQALLHP 897
Db 838 LANDFVFTLRLLHIAIKQLCPKIIIVERRMKOVFFFLFETISWLVAVGTTQALLHP 896
QY 837 LAIDFVFTLRLLHIAIKQLCPKIIIVERRMKOVFFFLFETISWLVAVGTTQALLHP 896
Db 837 LAIDFVFTLRLLHIAIKQLCPKIIIVERRMKOVFFFLFETISWLVAVGTTQALLHP 896
QY 898 HDORLEMIIPRRVLYRPLQIFGOIPLDEIDEARVNCSTHPLLEDSPSCSLANMLVIL 957
Db 898 HDORLEMIIPRRVLYRPLQIFGOIPLDEIDEARVNCSTHPLLEDSPSCSLANMLVIL 956
QY 897 HDORLEMIIPRRVLYRPLQIFGOIPLDEIDEARVNCSTHPLLEDSPSCSLANMLVIL 956
Db 897 HDORLEMIIPRRVLYRPLQIFGOIPLDEIDEARVNCSTHPLLEDSPSCSLANMLVIL 956
QY 958 LVTFLVTNLVNLMLLIAMFSYTFQVVOGNATMFWKFORNLIIVETHERPALAPFILL 1017
Db 958 LVTFLVTNLVNLMLLIAMFSYTFQVVOGNATMFWKFORNLIIVETHERPALAPFILL 1016
QY 957 LVTFLVTNLVNLMLLIAMFSYTFQVVOGNATMFWKFORNLIIVETHERPALAPFILL 1016
Db 957 LVTFLVTNLVNLMLLIAMFSYTFQVVOGNATMFWKFORNLIIVETHERPALAPFILL 1016
QY 1018 SHLSLTLRVFKKBAEHKEHLEBDLPDLDQVVTWETVQKENFLSKMEKRRDSEGEV 1077
Db 1018 SHLSLTLRVFKKBAEHKEHLEBDLPDLDQVVTWETVQKENFLSKMEKRRDSEGEV 1076
QY 1017 SHLSLTLRVFKKBAEHKEHLEBDLPDLDQVVTWETVQKENFLSKMEKRRDSEGEV 1076
Db 1017 SHLSLTLRVFKKBAEHKEHLEBDLPDLDQVVTWETVQKENFLSKMEKRRDSEGEV 1076

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QY 1078 LRKTAHRVDLAKYLGILREOEKRIKCLSEQINY 1111
Db 1077 LRKTAHRVDLAKYLGILREOEKRIKCLSEQSKY 1110
RESULT 7
Q8BS44 PRELIMINARY; PRT; 1030 AA.
ID Q8BS44
AC Q8BS44;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Transient receptor potential cation channel (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK035197; BAC28976.1;
FT NON_TER 1
SQ SEQUENCE 1030 AA; 116983 MW; DDBJ1B7DF238F402 CRC64;

Query Match 73.0%; Score 4445.5; DB 11; Length 1030;
Best Local Similarity 84.3%; Pred. No. 0;
Matches 856; Conservative 55; Mismatches 94; Indels 11; Gaps 3;

QY 151 LBAQEDPPVHYBEDDGGSGPLCSLDSNLSHFLVYEGPPEKG-DGLTELRLREKHS 209
Db 25 LBAQEDPPVHYBEDDGGSGPLCSLDSNLSHFLVYEGPPEKG-DGLTELRLREKHS 84
QY 210 BQAGYGGTSGIEIVLCLLVNGDPTLERISRAVEQAAPMLILVSGGIADVLAAVNO 269
Db 85 QRTGTGTCISQIPVCLLVNGDPTLERISRAVEQAAPMLILVSGGIADVLAAVNO 144
QY 270 PHLLVQVAKQKPKSPKHSFWMEDIVMTKLLQNTSHOHLITVDFEBOGSEELDTV 329
Db 145 PHLLVQVAKQKPKSPKHSFWMEDIVMTKLLQNTSHOHLITVDFEBOGSEELDTV 204
QY 330 ILKALVYACSHSGSEPDYIDELKLA VMDRVDAKSEIFNGDVEWKSCLDEEVMVDALV 389
Db 205 ILKALVYACSHSGSEPDYIDELKLA VMDRVDAKSEIFNGDVEWKSCLDEEVMVDALV 264
QY 390 SNKPEFVRLEFVNGADVADFLTYGRLOELYRSVSRKSLFDLQROKQEBARLTLAGLGTQ 449
Db 265 SNKPEFVRLEFVNGADVADFLTYGRLOELYRSVSRKSLFDLQROKQEBARLTLAGLGTQ 324
QY 450 QAREPPAGPAFSLHESRVYLQFLODACRGFYODGRRRAEKGPAPKPTGQKWLID 509
Db 325 QAREPPAGPAFSLHESRVYLQFLODACRGFYODGRRRAEKGPAPKPTGQKWLID 380
QY 510 LMGKSNEMPRDLPLMANVLQNRHEMATTFYAMQOEGVAAALAAACILKEMSHLETAEAR 569
Db 381 LMGKSNEMPRDLPLMANVLQNRHEMATTFYAMQOEGVAAALAAACILKEMSHLETAEAR 440
QY 570 ATREAKYERLALDFSECYSENSEARAFAALLVRRNRCSKTCTCLHATEADAKAFADGV 629
Db 441 ATREAKYERLALDFSECYSENSEARAFAALLVRRNRCSKTCTCLHATEADAKAFADGV 500
QY 630 QAFLTRIWMGDMAATPILRLGLAFLCFAVYTNLITFSEAPRTGLEDLQDLSLDT 689
Db 501 QAFLTRIWMGDMAATPILRLGLAFLCFAVYTNLITFSEAPRTGLEDLQDLSLDT 560
QY 690 KSPLYGQSRVEELVEAPRAQDGPRAVFLTRMKFMGAPVTVPLGNVVMYFAFLF 749
Db 561 KSPLYGQSRVEELVEAPRAQDGPRAVFLTRMKFMGAPVTVPLGNVVMYFAFLF 620

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QY 750 TVLLVDFRPPGSGSEVTVYFWVFTLVLEIRGSEFTDEBTHLVKKEFTLVYGDNNK 809
 DB 621 TVLLVDFRPPGSGSEVTVYFWVFTLVLEIRGSEFTDEBTHLVKKEFTLVYEDNNK 680
 QY 810 CDMVAIFELTVGTCGMLPSAFBAGTVALMPMTVTLTLHLFAHKGOLGKIIYVEM 869
 DB 681 CDMVAIFELTVGTCGMLPSAFBAGTVALMPMTVTLTLHLFAHKGOLGKIIYVEM 740
 QY 870 MDVFFELFELSVMLVAVYVTTQALLPHDGRLEWIFRRVLYRPYQIGQIPLDEIDA 929
 DB 741 MDVFFELFELSVMLVAVYVTTQALLPHDGRLEWIFRRVLYRPYQIGQIPLDEIDA 800
 QY 930 RVNCSHPLLEDSPSCPSLYANMVLILLVTLVTVNLVNLMLTAMSYTFQVQVQNA 989
 DB 801 RVNCSHPLLEDSPSCPSLYANMVLILLVTLVTVNLVNLMLTAMSYTFQVQVQNA 860
 QY 990 TMFMRFORNLYVEYHERPALAPRFLLSHLSTLRVVKGAHREHLEDDLPPLDQ 1049
 DB 861 DMFMRFORNLYVEYHERPALAPRFLLSHLSTLRVVKGAHREHLEDDLPPLDQ 920
 QY 1050 KVVWETVOKENFLSKMERKRRDSEGEVLRTAHRYVDFIAKYLGLREGEKIKCLESGQ 1109
 DB 921 KVVWETVOKENFLSKMERKRRDSEGEVLRTAHRYVDFIAKYLGLREGEKIKCLESGQ 980
 QY 1110 NYCSSLVSVADVLAQGGGPRSSOHGEGSOLVADHRGIDGWEQPGAGPPSDT 1165
 DB 981 NYCSSLVSMTDTLAPGTYTSSONCGRSOPASARDR-----EYLESGLPPSDT 1030

RESULT 8

Q8TD43 PRELIMINARY; PRT; 1214 AA.
 ID Q8TD43;
 AC Q8TD43;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Cation channel TRPM4B.
 GN TRPM4B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteleota; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Perraud A.-L., Scharenberg A.;
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF497623; AAM18083.1; -;
 DR Genew; HGNC:17993; TRPM4.
 DR InterPro; IPR002111; Cat channel_Trl.
 DR InterPro; IPR005821; Ion trans.
 DR Pfam; PF00520; ion_trans_1.
 DR Ionic channel; Transmembrane.
 KW ION CHANNEL; TRANSMEMBRANE.
 SQ SEQUENCE 1214 AA; 134300 MW; 76AD4452690ED8F5 CRC64;

Query Match 39.9%; Score 2430.5; DB 4; Length 1214;
 Best Local Similarity 45.4%; Pred. No. 2,3e-179;
 Matches 532; Conservative 177; Mismatches 352; Indels 111; Gaps 26;

QY 26 GEVNFSGSGKRGKRVVPSVAVPSVLPULLLAEMHLPAPNLVSLVGEOPFANKSWLR 85
 DB 76 GELDTGAGRKSNFLRLSDRTDPAVYSLVTRWGFAPNLVSVVLGSGGSPVLTQMLQ 135
 QY 86 DVLARGVLAASOSTAMVLTSLRVGLAHNGQAVRDHSLASTSTKRVVANGMSLGV 145
 DB 136 DVLARGVLAASOSTAMVLTSLRVGLAHNGQAVRDHSLASTSTKRVVANGMSLGV 194
 QY 146 LHRRLLEAQBDFPVHY-----PEDDGSQSGPLCSLDSNLSHFIVEPGRPGKGLTREL 200
 DB 195 RNRDRLINKSGSPARVWRGDPED--GVQFP---LDYVYSAFLVDDGTHCLGGENNF 249
 QY 201 RLRLKHSIQAGAGGCGTSGISIEIPVLCILVNDPNTLERISRAVEQADPMLILVSGGIA 260

DB 250 RLRLKHSIQAGAGGCGTSGISIEIPVLCILVNDPNTLERISRAVEQADPMLILVSGGIA 308
 QY 261 DVLALVNPVHLYV-----KVAEQKFEKFPKSHFSWEDIVMTKLLONITSHOHL 313
 DB 309 DCLATTLIED--TLAAGSGAROGEARDRIRRFPR-----GDLEVLQAOVERIMTRKELL 361
 QY 314 TVYDFEQSGSEELDTVILKALVKACKSHSQEPODYDELKLAIVAMDRIYAKSEIFNGDV 373
 DB 362 TVYSSE-DGSEEFITVILKALVKAC--GSSEASAYLDELRLAVANNRVDAQSEIFRQDI 418
 QY 374 EWSGCDLEWMDALVSNKPEFVFLVNGADVADPFLTYGRLOEYTRYSRSLPLDLO 433
 DB 419 QWRSHFLASLMDALNDRPEFVRLISHGLGHFTLPMRLAQDYSAAPSNSLRNLND 478
 QY 434 RKEBARLTLAGL--GTQOAREPPAGPAPFSLHESRVLKDFLOACRGFYODGPRGDR 491
 DB 479 QASHAGTKAPALKGAALRRP-----DVGHVRLMLGKMCAPRYTSGGAWDH 528
 QY 492 RAKEGPAPRPTGQKVLIDLNOKS-----ENFARDLFLVAVLQNRHEMATYFWAMQ 542
 DB 529 -----PGQOFGEVYLLSDKATSPSLDAGLQAPWSDULLWALLNRAQWAMYFWEMGS 583
 QY 543 EGVAAALAACTLKEMSHLETBAEAAATREA--KYERLADLSECTSNSRARPALLV 600
 DB 584 NAVSSALACCLLRVWARLEPDAEPAARKDLAFKEGCVDLFEGCYRSSSEVRAARLL 643
 QY 601 RNRCSKSTTCLHATEADAKAFPAHDGVQVAFTRIMGDMAGTPILRLGAPCFALV 660
 DB 644 RRCPLMGATCLQLMADARAFPAODGVOSLTICKMGDMASTPPIVALVLAFFCPLT 703
 QY 661 YTNLITF--SEBAPRLTGLEDLQDLSLDTESKPLYGQSRVEELVEAPRAQD----- 712
 DB 704 YTRLITFKSEEBEPREELE--FQMDSYINGGPGTADPAKFTLGVPRGGRGCCGG 761
 QY 713 --RGPRAVFLTRWKEFGAPTYVFLGVNVMFALFLPTVYLLVDFRPPGSGSEVTV 770
 DB 762 RCGGRRC--LRMWHFGAPVTTFMGVVSYLEFLFLFSRVLYVDFQAP--PGLLELL 816
 QY 771 LYFWFTLVLEIRGSEFTDEBT-----HLVKKFTLVYGDNNKCDMVAIFPI 819
 DB 817 LYFWFTLVLEIRGSEFTDEBT-----HLVKKFTLVYGDNNKCDMVAIFPI 876
 QY 820 VGVTCRMLPSAFBAGTVALMPMTVTLTLHLFAHKGOLGKIIYVERMKDVFPLFF 879
 DB 877 LGVGRRLRGLYHGRVLCIDFMVFTVRLHLHIFVNNQOLGPKIYIVGRMKMDVFPLFF 936
 QY 880 LSWLVAVYVTTQALLPHDGRLEWIFRRVLYRPYQIGQIPLDEIDARV--NCSTH 936
 DB 937 LGVWLVAAGVATEGILRPDSDFPSILRRVFYRPYQIFGOIPQEDMDVALMEHNSCSSE 996
 QY 997 PLLEDSF-----SCPSLYANMVLILLVTLVTVNLVNLMLTAMSYTFQVQVQNA 991
 DB 997 PGFWAHPRGAQAGTCSOTYANMVLILLVTLVTVNLVNLMLTAMSYTFQVQVQNSDL 1056
 QY 992 FMKFORNLYVEYHERPALAPRFLLSHLSTLRVVKGAHREHLEDDLPPLDQ 1042
 DB 1057 YWKQRYVLIHFEHRPALAPRFLIYSHLRLLRLQDCRRPSPOSSPALHFRVYLSKE 1116
 QY 1043 LPDPLDQVTVWETVOKENFLSKMERKRRDSEGEVLRTAHRYVDFIAKYLGLREGEKRI 1102
 DB 1117 -----AERKLITWESYHKNFLARARDKRESSESRKTSQVDLALKOLGHIHREYQRL 1172
 QY 1103 KLESQIYVCVSVSVADVLAQ-----GCP 1129
 DB 1173 KVLREVOQCSRVLGVAEALSRALLPPGGP 1204

RESULT 9

Q96L84 PRELIMINARY; PRT; 1040 AA.
 ID Q96L84;
 AC Q96L84;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)


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QY 413 GRLOELYSVSRKSLFLDLQKQSEARITLAGL--GTQQAEPAPGPPAFSLHEVSRVL 470
D 284 MRLAQVLSAAPSNSLRILNLDQASHAGTAKAPALKGAAELRPP-----DVGHVL 333
QY 471 KDFLODADRGFQODRPGDRRAEKGPAKRTGQKMLDLNQS-----ENPWRDL 521
D 334 RMLGKMCAPRYPSGGANDPH-----PGGFGESYVLLSDKATSPSLDAGLGQAPWSDL 388
QY 522 FLMAVLQNRHEMATYFMAWGOEVAALAAACKILKEMSHLETAEABARATREA--KYERL 579
D 389 LLMALLNRAQAMAYFMEGMSNAVSSALGACILLVMARLEPDAEABARRKDLAKFEGM 448
QY 580 ALDIFSECYSNSEARAFALLVRRNCWSKTTGLHATADAKAFPAHDQVQAFLTRIWMG 639
D 449 GVDLFEGECYSRSEVAARLLLRRCPLMGDATCTQLAMQADARAFPAQGVOSLTLQKWMG 508
QY 640 DMAACTPLRLILGALFCFALVYTNLITF--SEAPLRGLLELODLSLDTESPLYLGL 697
D 509 DMASTPLMALVLAFCFPLLYTRLITRKSEEBPTRELE--FMDMSVINGEGVTAD 566
QY 698 SRVEELVAPRAQD-----RGPRAVFLTRRKFMGAPVTVFLGNVWYFAFLFLF 749
D 567 PAETPLPGVPVROSGRPGCCGRCGRRC--LRKFHFMGAPVTLFMGNVSYLLFLDLF 623
QY 750 TYVLLVDRPPQSGSGEVLTYFWVFTLVLEIRQGFTEDEI-----HLVKK 798
D 624 SRVLLVDFOPAP--PGLELLLYFWAFLLCEBLQGLSGGGGSLASGPGPHASLSQR 681
QY 799 FTLVGDWANKCDMAVAFILFIVGTCRMLPSAFEGRTVLAAMDENVFTLRLIHFAIKQ 858
D 682 LRLVADSWNOCDLVALTCFLGVGCRLLPGLYHIGRTVLCLDFWVFTVRLHIFTVKQ 741
QY 859 LGPKIIVEREMKDVFFFLFSLVWLVAYGVTQALPHDGRLEWIFRRVLYRPLQIF 918
D 742 LGPKIVISKMKDVFFFLFGLVWLVAYGATBELLPDSDFSLIRRFYRPLQIF 801
QY 919 GOIPLDEIDEARV--NCSTHPLLEDSR-----SCPGLYANWLVILLVFLVTVNVL 970
D 802 GOIPOEDMDVALMEHNSCSSEBFWAHPGAQGTCSQYANWLVILLVFLVTVNVL 861
QY 971 MULLIAMSTYFOVYQNAATFMKQRYNLIVETHERPALAPPLLSLTLRLRVFK 1030
D 862 VULLIAMSTYFGKQNSDLYWKAORYLRIEFHSRPALAPPLFVISHLLRLQLCR 921
QY 1031 -----BAEHKREHLERDLPDLQKVTWVQENFLSKMEKRKRSSEGVLAKT 1081
D 922 PRSPOSSPALHEHRYVLSKE--AEKKLLTWESVHKENFLADARCKRESDESLERT 977
QY 1082 AHRVDFIAKYLGLREDEKRIKLESQINYS 1113
D 978 SQKVDLALKOIGHIREYQRLKVLEREVOQS 1009

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RESULT 11
Q8BLM7
ID Q8BLM7 PRELIMINARY; PRT; 945 AA.

AC Q8BLM7;
DT 01-MAR-2003 (Tremblrel. 23. Created)
DT 01-MAR-2003 (Tremblrel. 23. Last sequence update)
DE 01-MAR-2003 (Tremblrel. 23. Last annotation update)
DE Similar to TRP-related cation influx channel.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N. A.
RC STRAIN=C57BL/6J; TISSUE=Cortex;
RX MEDLINE=2354683; PubMed=12466851;
RA THE FANTOM Consortium;
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT Analysis of the mouse transcriptome based on functional annotation of

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RT 60,770 full-length cDNA.
RL Nature 420:563-573 (2002).
DR EMBL; AK044094; BAC11771.1;
SQ SEQUENCE 945 AA; 105526 MW; B7261C0A3688668B CRC64;

Query Match 33.7%; Score 2051; DB 11; Length 945;
Best Local Similarity 45.6%; Pred. No. 4,8e-150;
Matches 453; Conservative 141; Mismatches 276; Indels 124; Gaps 27;

QY 100 GAWILTSALRGILABHQVQARHDSIASTSKVAVNAGMSLQGVLRHRLIEAQDPP 159
D 4 GAWIVTGLTGTHGIVHGVAVRDHQTASTGSS--KVAVAGVAPWGVNRRDMLINKGSP 62
QY 160 VHY-----PEDDGSQGPLCGLSDNLSHFILVERPCPPGQGLTELRLEKHSIORAG 214
D 63 ARYMRGPED--GVEFP--LDVNSAFVLVDGTYRLOGENRFRLPESYVAQKXTG 117
QY 215 YGTTGSIETPVLCLLVNGDPNTLERISRAVEQAAPMLLVSGGSIADVLAALVNPMLLV 274
D 118 VGGTG-IDIPVLLLLIDGDEKMLKRIEDATQAQPLCLLVAGSGGAADCLVETLED--TLA 174
QY 275 P-----KVAEKQPKKEFPKSHSWEDIYVWTKLONITSHOHLTYTDEQSGSELD 327
D 175 PGSGGLRGEARDEIRRYFPK-----GPEVLQAOVERIMTRKELTYSSB--DSBEP 228
QY 328 TVILKALVKAACKSHSOEPODYLDLKLAVANDVIAKSEIFNGDVEKSCDLEEWYDA 387
D 229 TIVRALVAKC--GSSESAVLDELRLAVANRRDIAOSELPFGDIOHRSFHEASLMDA 286
QY 388 LVSNKPEFVRLFVNGADVADFLTYGRLOELYSVSRKSLFLDLQKQSEARITLAGLG 447
D 287 LLNRPPEFVRLISHGLSHGFLTPVRLAQLYSAVSPNSLRILNLDQASH----- 336
QY 448 TQQAEPAPG-----PRASLHEVSRVLODADCRGF-----ODCRPDR 490
D 337 ASSSKSPVNGTVELRPP-----NVGOVLRLLAETCAPRPARNTRDSYLGODHREND 390
QY 491 RRAEKGPAPRTGQKMLDLNQS-----SENPWRDLFLMAVLQNRHEMATYFMAWGO 542
D 391 -----SLMDANKOPSTDASEQAQPMEDLILMALLNRAQNAIYFWEKGS 436
QY 543 EGVAAALAAACKILKEMSHLETAEABARATRE--AKYERLALDIFSECYSNSEARAFALLV 600
D 437 NSVASALGACILLVMARLESEABEARRDLATFSPMSVDLGECHNSEEBAARLL 496
QY 601 RANRCWSKTTGLHATADAKAFPAHDQVQAFLTRIMGMAAGTPILRLIGALFCFALV 660
D 497 RRCPLMGEATCTQLAMQADARAFPAQGVOSLTLQKWMGEMDSTTPVALLLAFCCPLI 556
QY 661 YTNLITF--SEAPLRGLLELODLSLDTESKPLYLGLQSVLEELVAPRAQGRPRAY 718
D 557 YTNLIVRKSEEBPTQOLD--FMDSSINGAGPGTVEPAKVALE--RRORRRPGAL 612
QY 719 F--LITRMKFMGAPVTVFLGNVWYFAFLFETVYLVDFRPPQSGSEVTLFVWV 775
D 613 CCGKFSKMSDFWKAFTAFILGNVSYLLFLFLFAHLVLDFOYTK--PSSELLTYMA 670
QY 776 FTLVLEIRQCF-----FTDEDTHLVKKFTLYVGDWANKCDMAVAFILFIVGTC 824
D 671 FTLLCEELRQGLGGWMSLASGGRPRAPLRHRLHLYSDPWNQCDLALTCFLAGVC 730
QY 825 RMLSAFEAGRTVLAAMDENVFTLRLIHFAIKHOLGKRIYVENMDVFFFLFSLVW 884
D 731 RLTPGLFDLGRITVCLDFPMFTLLRLHLIFVNNKOLGPRIVVSKMDVFFFLFCVL 790
QY 885 VAVGVTTQALLPHDGRLEWIFRRVLYRPLQIFGQIPLDEIDEARV--NCS-----T 935
D 791 VAVGVATEGLLRPDGRSLPSILRRVFRPLQIFGQIPOSEMDVALMIPNGCSMERGSA 850
QY 936 HPLLEBSP--SCPGLYANWLVILLVTVNVLNMLLIAMSTYFOVYQNAATMF 992
D 851 HP-----GPAVAGCVCVQYANWLVILLVFLVLANILLMLLIAMSTYFSKVHGNSDLY 906

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QY 993 WKFORXNLIYVHERPALAPPELLSHSLTLRR 1026
DB 907 WKQGRYSILREPHSRPALAPPELLIICHVSVRK 940

RESULT 12
QY 091YD4 PRELIMINARY; PRT: 1507 AA.
AC 091YD4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Transient receptor potential channel 7 (fragment).
GN TRP7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/c;
RA Kashiuba V.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ344343; CAC69081.1;
DR InterPro; IPR002311; Cat_channel_TrpL.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR002052; N6_Mtase.
DR InterPro; IPR000086; NUDIX_hydrolase.
DR Pfam; PF00520; Ion_trans; 1.
DR Pfam; PF00293; NUDIX; 1.
DR PROSITE; PS00092; N6_MTASE; 1.
DR Ionc channel; Receptor; Transmembrane.
KM NON_TER 1507 1507
SQ SEQUENCE 1507 AA; 172364 MW; 86E552DE25939785 CRC64;

Query Match 33.2%; Score 2024; DB 11; Length 1507;
Best Local Similarity 39.1%; Pred. No. 1,3e-147;
Matches 449; Conservative 133; Mismatches 386; Indels 120; Gaps 22;

QY 26 GEVNFSGSKGKGFVVPVSPVAPSVLFDLLAEWHLPAFNLVSLVGEQPPAKMSWR 85
DB 127 GIVFIDLSQKVGKVRVSDPTFSSVITLMTQHWGLDVPNLLISVTGAKNFMMLRLK 186
QY 86 DVLRKGLVRAAGSTGMIWLTSLRVGLARHVGQAVPDHSLASTKRVRAVAVMABLSGV 145
DB 187 SIFRRGLVRAVQTGAMITGSGHTGMQVGAVDPSLSSCKGGEVITTGVAWGTI 246
QY 146 LHRRIIEBAQEDPPVHYPPDDGSGGPLCSLDNSLHFLIVGPPGKGDGLTELRLRL 205
DB 247 HNRBGLIHPWGGFPAEYMLDDEG-QGNLTCLDSNHSHFILVDGTGQGVETPLTKLE 305
QY 206 KHISEORAGYGTGSIPIVLCILVNGDPNTERISRAVEQAAPWILVSGGDIADVLA 265
DB 306 KFISEQTKREGGV-AIKIPICVVLGGPGLTHTIYNAINNGPPCVIVEGSGVADVIAQ 364
QY 266 LVNQF--HLIVPVAKQ--FEKFPKSHFSEWDIVRTKLIQNTSHOHLITVDFEQ 320
DB 365 VATLPVSEITISLIQKLSIFQEMFET--FTENOIVEMTKKIQDIVRRQLITIFRECK 422
QY 321 EGSEEDTVTLKALVAKCSHSEQPDYLD-ELKLAAMRVNIAKSEIFNGDVENWSCD 379
DB 423 DGGDDVDVALIQLALAKRSQDHFHGNMHDOLKLAAMRVNIAKSEITTDQMOKPAD 482
QY 380 LBEVNVDAIVSNKPEFVRLFVNDGADVADFLYGRLOELVRSVRSKSLFDLLQR-KQEE 438
DB 483 LHPMMTAAALISNKPDEFRLFLKGVRLKEVMTDILCTVENLEPSCLPFSKLOKVLAEE 542
QY 439 ARITLGLGTQARPPAGPARPSLHVSRYLKDPLDACKRGYQDGRPDGRRAE---- 494
DB 543 QRLAFA-----SATPRLHMHVAVQLRELLDSTQLLYPRDRYDRPLSMTPV 591
QY 495 -----KQPAKPTGQ-KWILLDNQKSENPMDLFLMVLQVRHEMATYFNAMGQ 542

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DB 592 HIKLVNGVSLRSYKSTGHTFTID-----PVRLLIWAVIQNRELAGIIMASQ 644
QY 543 EGVAALAAACILKEMSHLE--TEABARATREAKYERLALDLPSECSNSEARAFALLY 600
DB 645 DCTAALAKSKILKELSEEDTDSSEMLALADEFERAIGVTECKRKEBRKOLLY 704
QY 601 RRNRCSKTTICILHATEADAKAFPAHDGVAFLTRIMWGDMAAGTPILRLGAFCLFALY 660
DB 705 RVSEAMGKTTIQLALBAKDKMFVSHGIGQFLFTVMWGOCLVDNGLIRIILCMALFPLL 764
QY 661 YTNLITPSEEARPLRTGLDLDLDDLSLDTKSPBYGLQSRVEELYAPPAQDGRRAFL 720
DB 765 FTGISFPEK-----RLQALCRPAV----- 785
QY 721 LTRMKFGAVTVTELGWVWVFAFLFLTYVLVDPFRPPGSPGSEPTLYFVFTLYL 780
DB 766 ---RAFNAPVAFVFMNIIISYFAFLCLFAVLMVDFP---SPSCYLLIYMLFSLVC 838
QY 761 EIRGQFTDED-THLVKKFTLYVGDNNKCDMAVAFPLIVGTCRMLPSAEAGRTVLA 839
DB 839 BETROYLYDPDGGCLMAGASLYFSDPNNKLDVGAILLFIYGLTCRLIPATLYPGRIILS 898
QY 840 MDEFVFTLRLIHIFAIHKQLGPKTIIVERMKDVFPLFPLSVLWLVANGVTTQALLPHPD 899
DB 899 LDFIMFCLRLMHIFTSKTLGPKTIIVKRMKDVFFFLFLAVWVSGVAKQAILIHNE 958
QY 900 GLEWIFFRVLRYRPLQIFGQIP--LDLIDEARVNC--THPLLEDSPPSCPS----- 948
DB 959 SRVDWIFGVVYHSLTTFGQIPYIYDGNFSMDQCSPNGTDPY--KPKCPESDWTGQ 1014
QY 949 --LVANMVIILLVTLVTLVTLVNLNLIAMFSYTFQOVGNATFMFKQRYNLIVERYE 1006
DB 1015 AAPPEWTLVTLCLCYLIPANILLNLIAMNVTFOEQEHTDQIMKQRHDLLEYHG 1074
QY 1007 RPALAPPELLSHSLTLRVKFEKAHREHLEBDLPDLQKYVTEVQENFSLQM 1066
DB 1075 RPPAPPPELLSHSLTLRIKRYLKIPAKHKQIKKLEKNEETALLSWLYKEVYLOQ 1134
QY 1067 EKRRRDSGEVLRKTAHVRDFAKYL-----GGLRQEKIKICSQINCSVLVSSV 1119
DB 1135 QYQQAQRPQKIQDISEKVDIVDLDMDQVKSSTEO--RLASLEQVTOVTALHMI 1192
QY 1120 ADVLAQGG 1127
DB 1193 VTTLKDSG 1200

RESULT 13
QY 08R4D5 PRELIMINARY; PRT: 1104 AA.
AC 08R4D5;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE TRP ion channel TRPM8 (Transient receptor potential Ca++ channel TRPM8)
GN TRPM8 OR TRPM8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA MEDLINE=21890731; PubMed=11893340;
RA Peier A.M., Moggridge A., Hergarden A.C., Reeve A.J., Andersson D.A.,
RA Story G.M., Barley T.J., Dragon I., McIntyre P., Bevan S.,
RA Patapoutian A.; that senses cold stimuli and menthol.";
RT "A TRP channel that senses cold stimuli and menthol.";
RL Cell 108:705-715(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;

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RA Tsavalier L., Laus R.:
 RT "The murine homologue of TRPM8 (Trpm8) gene: cloning, sequencing and
 tissue distribution."
 RL Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF481480; AAL79553.1; -
 DR EMBL: AY095352; AAM23261.1; -
 DR MGI: 2181435; Trpm8.
 DR InterPro: IPR002111; Cat_channel_TrpL.
 DR InterPro: IPR005821; Ion_trans.
 DR Pfam: PF00520; Ion_trans_1.
 DR Ionic channel: Receptor: Transmembrane.
 KW
 SQ SEQUENCE 1104 AA; 127709 MW; 1685D6FEBD2BE96D CRC64;

Query Match 25.9%; Score 1578; DB 11; Length 1104;
 Best Local Similarity 33.4%; Pred. No. 3,4e-113;
 Matches 374; Conservative 207; Mismatches 392; Indels 148; Gaps 24;

26 GEVNGSGGKRGKRVVPVSGVAVLFDLLLAEMHLPAPNLVSLVGEOPFANKSWLR 85
 DB 104 GDIOFETLGKK-GKYLRLSCDTSBETLYELLTQHMLKTPNLVSVTGAKNFKALPKPRM 162
 86 DVLRKGLVKAAGSTGAMILTSALRGVLAHVGAVRDHSLASTSTKRVAVAGMASLGRV 145
 DB 163 KIFSR-LIYIAOSKAMILTGTHYGLMKYIGEVVDNTI-SRSEENIYALGIAAMGV 220
 146 LHRRLIEAOD---FVHYPEDDGSQGLCSLDSNLSHFILVEPGPGKGGTLETRL 202
 DB 221 SNRDLIRSCDDEGHFSAQYIMD-FTRDPLIYIDNNHTHLLVNGCHGHFTVEAKLRN 279
 203 RLEKHISE---ORAGYGTGSIIEIPVCLLVNGDPNTLERISRAVEQAAPMLILVSGGI 259
 DB 280 QLEKISERTSDSNYGG---KIPVCFAGGREGTEIKALINTSVKSKIPCVVVEGSGOI 335
 260 ADVLAALVNQPHILVPKVAEKOFKEKFPSS-KHFSMEDIVRTKXLLONTSHQHLTYVD 317
 DB 336 ADVIASLVEVEDVLTSSWVKEVLPRTVSRLPEEBESITKMLKEILSSHLTYIK 395
 318 FEOGSEELDTVILKALVAKCKSHQEPDYLDELKLAVAMRDVIAKSEIFNGDVEWKS 377
 DB 336 MEEADDELVSNAISVALYKAFSTNQDKNNWGQKLLLENQDLASSEIFITNRRMES 455
 378 CDLEEVNDAVLSNKPFRVFLVDNGADVADFLTYGRLOELVRSYRSKSLFDELQ---R 434
 DB 456 ADLOEVMTALIKDRPKFVRLFLENGNLQKELTNEVLETF-STHFTSLVRYNLQIAKN 514
 435 KOEERLTLAGCTQOARPRAPRPFSLHESRVLKQLOACGPFODGPRGRRAE 494
 DB 515 SYNDLALT---VWKLVANFR---RSFWKEDR----- 540
 495 KGPARKPTGOKWLDLNOKSENPRDLFLMAVLQNRHEMATYFMAOGEGVAAALAAKI 554
 DB 541 ---SRREDLVDELHNASLITRRHPLDALFIMALQKKELSKIWTGCTIALAAGAKL 597
 555 LKESHSLETEAARATREBA-KYERLALDFSECSYNSSEARAFALLVRRNCWSTTCL 612
 DB 598 LKTLAKKNDINAAESEBELANEYETRAVELTECSNDEDELABOLLYVSCAAMGSNCL 657
 613 HLATEADAKAPFAHNGVQAFELTRIMWGDMAACTPIRLGLGALCALVYTNLITSEAP 672
 DB 658 ELAVEATDOHFIAQPGVQNFISKQYGEISRTKWKIILCLFIPLVGGGIVSFRKK-- 715
 673 LRTGLEDDLDLSDTEKSPLYGLQSRVELEAPRAQDGRPAVFLITTRARKFWGAPV 732
 DB 716 ---PDKHKK-----LLMYVALEFTSPF 735
 733 TVPLGNVVMYFAFLFTYVLLVDRPPQSGSEVTLVFWVFTVLVEIRQGFTEED 792
 DB 736 VVFSNNVVFYIAFLFLFVLLMDHVSBH---TEPLIYALVFLFCDEVQWYMGV 792
 793 THLVKKFTLVYGDNNKCDMVAIEFLIVGTCRM---LPSAEARTVLAMDFWFTLRL 849
 DB 793 ---YFTDLNVMDDTGLGFYFIAGIVFRLHSSNKSLSYSGRVIFCLDYIIIFTLRL 843

QY 850 IHIFAIHQLOPKIIVVERMKVDFFFLFSLVWLVAVGTTQALLHPDGLNFIPIRV 909
 DB 844 IHIFVSNLBPBKIMQRLMIDVFFFLFVAVVAVGARGOGLRONEGRMWIRFSV 903
 QY 910 LYRPLQIFGQIPDEIDARVNC-----THPLLE-DSPCSPSLYANWLVILLY 960
 DB 904 IYEPYLAIFGVPSD-VDSITYVDHCTFSGNSKPLCEVDEHNLPR-FPEWITIPVLC 961
 QY 961 TELVTVNLVNLMLIAMFSYTFQVQGNATFMFKFORNLIVYERPALAPPIILSHL 1020
 DB 962 IYMLSTNLVNLVNLVAMGYVIGVQENNDQVKFORFLVQVQCNRLNIPPFVFAV 1021
 QY 1021 SLTLARVKEAENKREHLEBDLPDQKVYVETVQENFLSPMEKRRRDEGEVLAK 1080
 DB 1022 YVWVKKCFKCCCKEKMSNACFPENEDNETLAMEGVKENVLYKINTKANDNS----- 1075
 QY 1081 TNRVDFIAKVLGLRQEKIKCLESDIYNCVSVSSVAD 1121
 DB 1076 -----EEMRHRFRLDSKXLDNLKSLKEIAN 1101

RESULT 14

Q8R455 PRELIMINARY; PRT; 1104 AA.

AC Q8R455;
 DT 01-JUN-2002 (Tremblrel; 21, Created)
 DT 01-JUN-2002 (Tremblrel; 21, Last sequence update)
 DT 01-OCT-2002 (Tremblrel; 22, Last annotation update)
 DE Cold/menthol receptor 1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Trigeminal ganglion;
 RX MEDLINE=21877404; PubMed=11882888;
 RA McKemy D.D., Neuhauser W.M., Julius D.;
 RT "Identification of a cold receptor reveals a general role for TRP
 channels in thermosensation."
 RL Nature 416:52-58(2002).
 DR EMBL: AY072788; AAL68394.1; -
 DR InterPro: IPR002111; Cat_channel_TrpL.
 DR InterPro: IPR005821; Ion_trans.
 DR Pfam: PF00520; Ion_trans_1.
 KW Ionic channel; Receptor; Transmembrane.
 SQ SEQUENCE 1104 AA; 127651 MW; 0FBEDD11FC025D09 CRC64;

Query Match 25.7%; Score 1563.5; DB 11; Length 1104;
 Best Local Similarity 34.0%; Pred. No. 4,6e-112;
 Matches 375; Conservative 205; Mismatches 395; Indels 129; Gaps 25;

QY 26 GEVNGSGGKRGKRVVPVSGVAVLFDLLLAEMHLPAPNLVSLVGEOPFANKSWLR 85
 DB 104 GDIOFETLGKK-GKYLRLSCDTSBETLYELLTQHMLKTPNLVSVTGAKNFKALPKPRM 162
 QY 86 DVLRKGLVKAAGSTGAMILTSALRGVLAHVGAVRDHSLASTSTKRVAVAGMASLGRV 145
 DB 163 KIFSR-LIYIAOSKAMILTGTHYGLMKYIGEVVDNTI-SRSEENIYALGIAAMGV 220
 QY 146 LHRRLIEAOD---FVHYPEDDGSQGLCSLDSNLSHFILVEPGPGKGGTLETRL 202
 DB 221 SNRDLIRSCDDEGHFSAQYIMD-FMRDPLIYIDNNHTHLLVNGCHGHFTVEAKLRN 279
 203 RLEKHISE---ORAGYGTGSIIEIPVCLLVNGDPNTLERISRAVEQAAPMLILVSGGI 259
 DB 280 QLEKISERTSDSNYGG---KIPVCFAGGREGTEIKALINTSVKSKIPCVVVEGSGOI 335
 QY 260 ADVLAALVNQPHILVPKVAEKOFKEKFPSS-KHFSMEDIVRTKXLLONTSHQHLTYVD 317
 DB 336 ADVIASLVEVEDVLTSSWVKEVLPRTVSRLPEEBESITKMLKEILSSHLTYIK 395
 QY 318 FEOGSEELDTVILKALVAKCKSHQEPDYLDELKLAVAMRDVIAKSEIFNGDVEWKS 377


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Db      396 MEADGEVSSAISYALYKAFSTNEDKXNMNGOLLEMMQDLASDEITHRRMWS 455
Qy      378 CDLEEVMDALVSNKPEFRLFVDNGADVADLTGRLQLOELYSRSRKLDELLO--R 434
Db      456 ADLOEVMFALIKDPRKPFVRLFENGMLNOKFLEIVELF-STHFSTLVYRNQIANK 514
Qy      435 KOEBARLTLAGTQOAREPPAPPAFSLHEYSRVLDLOACRGFYDDGRRRAE 494
Db      515 SYNDALTF-----VKKVANR-----RSFKEDR----- 540
Qy      495 KGPAPKPTGQKMLDLNOKSENPMWDLFLMAVLONRHEMATYFWAMGEGVAAALAAKCI 554
Db      541 ----SSREDDELHDLASTLTRHPLOQLFWAILQNKKEISKVIWEGTKCTIALGASKT 597
Qy      555 LKEMSHLETAEARATREA--KYETLADLDFSECSYNSBARAFALLVRRNCWKTTL 612
Db      598 LKTLAKVKNDINNAAGESELANEYETRAVELFTECYSDEDLAEOLLYVSCAMGSGNCL 657
Qy      613 HLATEADAKAFADGVQAFLTRIMWGDMAAGTPILRLGALFCFALVYTNLTTFSEBAR 672
Db      658 ELAVEATDQHFLAQPGVQNFSLKQWYGETSRDTKMKITLCFLIFVGGGLVSPFK-- 715
Qy      673 LRTGLDLDLSDTEKSPLYGLOSREVELVEAPRAQDGRGPAVELLTRMRKFWGAPV 732
Db      716 -----PIDCHK-----LMWYVAFSTSPF 735
Qy      733 TVPLGNVWYFAFLFTYVLVLDPRPPQSGSEVTLFVWFTLVLEIRQGFTEDE 792
Db      736 VVFSNMVVFYIAFLFLFAYVLLMDFHSVPH--TPELILYALVFVFCDEVQWYNGVN 792
Qy      793 THLVKFTLYVGDNMWCMVAIFLFIYVTCGM--LPSAFAGRTVLAMDPMVTLRL 849
Db      793 -----YFTDLNMVMDTLGLFTIAGIVRLSHSSNKSLSYSGVITCLDITITLTL 843
Qy      850 IHIPIAHKOLGPKIIVVERMKDVFFFLFSLVWLVAVGTTQALHPHDLGLWIFRRV 909
Db      844 IHIFTSRNLGPKIIMLQMLDIVFFFLFPAVMVAVFAGARGILRQNEGRWIFRSY 903
Qy      910 LTRPYIQTGQIPLDEIDARVNC-----THPLLE-DSPECSLYAMVLLVLLV 960
Db      904 IVEPYLAMEGVPSD-VDSITTYDFSHCTFSGNESKPLCVELDEYNLPR-FPEWITPLVC 961
Qy      961 TELLVNVLNMLLMFSYTTPOVQGNATMFKPQRYNLIVEYHRRPLAPPILSLH 1020
Db      962 IYMLSTNILLVNLVLMFGLTYGIVGENDQWKFQRYFLVQETCYCRMLNIPFFVFAIF 1021
Qy      1021 SLTLREVPFKEAEHREHLERDLDPDLQKVVTWETVOKENFLSKMEKRRDSEGEVLR 1080
Db      1022 YWVVKKCFCCCKEKTESACCFRMEDEBETLAMGVMKENYLVKINTYANDV-AEMKH 1080
Qy      1081 TAHRVDFIKYLGG-LREQEKIK 1103
Db      1081 RFRQDLTKLNDLKLKEIANKIK 1104

RESULT 15
Q8TDx8 PRELIMINARY; PRT; 1095 AA.
AC Q8TDx8;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE LTRPC6.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN (1)
RP SEQUENCE FROM N.A.
RA Sano Y., Inamura K., Miyake A., Mochizuki S., Yokoi H., Kitada C.,
Nozawa K., Matsushima H., Furutachi K.,

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RT      "Molecular cloning of a novel member of LTRP channel family, LTRPC6."
RL      Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AB061779; BAB6135.1; -.
DR      InterPro; IPR002111; Cat_channel_Trlp.
DR      InterPro; IPR005821; Ion_trans.
DR      Pfam; PF00520; Ion_trans; 1.
KW      Ionic channel, Transmembrane.
SQ      SEQUENCE 1095 AA; 126634 MW; 3BA3BD4CF420361 CRC64;

Query Match      25.6%; Score 1559.5; DB 4; Length 1095;
Best Local Similarity 34.1%; Pred. No. 9,2e-112;
Matches 377; Conservative 203; Mismatches 394; Indels 131; Gaps 27;

Qy      26 GEVNGSGGKRGKGVVRSVGVAPSEVLPDLLEAEMHLPAPNLVSLVGEQPFAPKSMYLR 85
Db      95 GDIGFETLQK-GKIRISCDTDAELIVELLQHNHKLTPNLVISTGAKNFALKPRNR 153
Qy      86 DVLARGLVKMAOSTGAMILTSALRVGLARHGQAVRDSLASTSTKRVVAVGASLGRV 145
Db      154 KIFSR-LIYIAQSGKAMILLGTGTHYGLMKYIGEVRDNTI-SRSSEENIVAIIGIAMGV 211
Qy      146 LHRRLLE--EAQEPFPHIFEDDGSQGLCSLDSNLSHFTLVPRPGKGDGLTELRL 202
Db      212 SNRDLIRNCABEGYFLAQYIMDD-FTRDPLYLIDNNHTHLVLVNGCHGPTVEAKLN 270
Qy      203 BLEKHISE---ORAGYGTGSIIEIPVLCILVNGDENTLERISRAVEOAPMFLVSGGI 259
Db      271 QLEKTISETTIDSNYCG---KIPVCFAGCGGETLKAINTSKNKIPCVVSGSGI 326
Qy      260 ADVLAALVNPQLVLPVKAQKQKFKPS--KHFSMEDIVRWTKLLQNTSHOHLITVYD 317
Db      327 ADVIASLVEVEDALTSNAKKEKLVRFPTVSRLEPEETESWIKMLKELECSHLITVYK 386
Qy      318 FEQGESELDYTIKALVYKACKSHQEPQDYIDELKLVAMRVLIASEINQDQWMS 377
Db      387 MEADGEVSSAISYALYKAFSTSDOKNMNGOLLEMMQDLANDEITNDRMWS 446
Qy      378 CDLEEVMDALVSNKPEFRLFVDNGADVADLTGRLQLOELYSRSRKLDELLO--R 434
Db      447 ADLOEVMFALIKDPRKPFVRLFENGMLNKRKLTHDVLELF-SHFSTLVYRNQIANK 505
Qy      435 KOEBARLTLAGTQOAREPPAPPAFSLHEYSRVLDLOACRGFYDDGRRRAE 493
Db      506 SYNDALTF-----VKKVANR-----RGFRKEDNGDEMDI 539
Qy      494 KGPAPKPTGQKMLDLNOKSENPMWDLFLMAVLONRHEMATYFWAMGEGVAAALAAK 553
Db      540 E-----LHDVSPITRHPLOQLFWAILQNKKEISKVIWEGTKCTIALGASK 587
Qy      554 LKEMSHLETAEARATREA--KYETLADLDFSECSYNSBARAFALLVRRNCWKTTC 611
Db      588 LKTLAKVKNDINNAAGESELANEYETRAVELFTECYSDEDLAEOLLYVSCAMGSGN 647
Qy      612 HLATEADAKAFADGVQAFLTRIMWGDMAAGTPILRLGALFCFALVYTNLTTFSEBAR 671
Db      648 LEAVEATDQHFLAQPGVQNFSLKQWYGETSRDTKMKITLCFLIFVGGGLVSPFK-- 706
Qy      672 PLRTGLDLDLSDTEKSPLYGLOSREVELVEAPRAQDGRGPAVELLTRMRKFWGAP 731
Db      707 -----PVDCHK-----LMWYVAFSTSPF 725
Qy      732 TVPLGNVWYFAFLFTYVLVLDPRPPQSGSEVTLFVWFTLVLEIRQGFTEDE 791
Db      726 VVFSNMVVFYIAFLFLFAYVLLMDFHSVPH--PEELVLYSLVFLFCDEVQWYNGVN 782
Qy      792 DTHLVKFTLYVGDNMWCMVAIFLFIYVTCGM--LPSAFAGRTVLAMDPMVTLRL 848
Db      783 N-----YFTDLNMVMDTLGLFTIAGIVRLSHSSNKSLSYSGRVIFCDYIIFTLR 833
Qy      849 LHIPIAHKOLGPKIIVVERMKDVFFFLFSLVWLVAVGTTQALHPHDLGLWIFRR 908
Db      834 LIHIFTSRNLGPKIIMLQMLDIVFFFLFPAVMVAVFAGARGILRQNEGRWIFRS 893

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